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(54) Title: KUNITZ DOMAIN POLYPEPTIDE ZKUN8

(57) Abstract: Proteinase inhibitors comprising a Kunitz domain are disclosed. The Kunitz domain comprises a motif of amino acid residues as shown in SEQ ID NO:7, wherein the sequence is at least 90 % identical to residues 328 through 378 or 386 through 436 of SEQ ID NO:2. Also disclosed are methods for producing the proteinase inhibitors, and expression vectors and cultured cells that are useful within the methods. The proteinase inhibitors may be used as components of cell culture media, in protein purification, and in certain therapeutic and diagnostic applications.

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Description

5

## KUNITZ DOMAIN POLYPEPTIDE ZKUN8

## BACKGROUND OF THE INVENTION

In animals, proteinases are important in wound healing, extracellular matrix destruction, tissue reorganization, and in cascades leading to blood coagulation, fibrinolysis, and complement activation. Proteinases are released by inflammatory cells for destruction of pathogens or foreign materials, and by normal and cancerous cells as they move through their surroundings.

The activity of proteinases is regulated by inhibitors; 10% of the proteins in blood serum are proteinase inhibitors (Roberts et al., Critical Reviews in Eukaryotic Gene Expression 5:385-436, 1995). One family of proteinase inhibitors, the Kunitz inhibitors, includes inhibitors of trypsin, chymotrypsin, elastase, kallikrein, plasmin, coagulation factors XIa and IXa, and cathepsin G. These inhibitors thus regulate a variety of physiological processes, including blood coagulation, fibrinolysis, and inflammation.

Proteinase inhibitors regulate the proteolytic activity of target proteinases by occupying the active site and thereby preventing occupation by normal substrates. Although proteinase inhibitors fall into several unrelated structural classes, they all possess an exposed loop (variously termed an "inhibitor loop", a "reactive core", a "reactive site", or a "binding loop") which is stabilized by intermolecular interactions between residues flanking the binding loop and the protein core (Bode and Huber, Eur. J. Biochem. 204:433-451, 1992). Interaction between inhibitor and enzyme produces a stable complex which disassociates very slowly, releasing either virgin (uncleaved) inhibitor, or a modified inhibitor that is cleaved at the scissile bond of the binding loop.

One class of proteinase inhibitors, the Kunitz inhibitors, are generally basic, low molecular weight proteins comprising one or more inhibitory domains ("Kunitz domains"). The Kunitz domain is a folding domain of approximately 50-60 residues which forms a central anti-parallel beta sheet and a short C-terminal helix. This characteristic domain comprises six cysteine residues that form three disulfide bonds, resulting in a double-loop structure. Between the N-terminal region and the first beta strand resides the active inhibitory binding loop. This binding loop is disulfide bonded through the P2 Cys residue to the hairpin loop formed between the last two beta

strands. Isolated Kunitz domains from a variety of proteinase inhibitors have been shown to have inhibitory activity (e.g., Petersen et al., Eur. J. Biochem. 125:310-316, 1996; Wagner et al., Biochem. Biophys. Res. Comm. 186:1138-1145, 1992; Dennis et al., J. Biol. Chem. 270:25411-25417, 1995).

5 Proteinase inhibitors comprising one or more Kunitz domains include tissue factor pathway inhibitor (TFPI), tissue factor pathway inhibitor 2 (TFPI-2), amyloid  $\beta$ -protein precursor (A $\beta$ PP), aprotinin, and placental bikunin. TFPI, an extrinsic pathway inhibitor and a natural anticoagulant, contains three tandemly linked Kunitz inhibitor domains. The amino-terminal Kunitz domain inhibits factor VIIa,  
10 plasmin, and cathepsin G; the second domain inhibits factor Xa, trypsin, and chymotrypsin; and the third domain has no known activity (Petersen et al., *ibid.*). Aprotinin (bovine pancreatic trypsin inhibitor) is a broad spectrum Kunitz-type serine proteinase inhibitor that has been shown to prevent activation of the clotting cascade. Aprotinin is a moderate inhibitor of plasma kallikrein and plasmin, and blockage of  
15 fibrinolysis and extracorporeal coagulation have been detected in patients given aprotinin during open heart surgery (Davis and Whittington, Drugs 49:954-983, 1995; Dietrich et al., Thorac. Cardiovasc. Surg. 37:92-98, 1989). Aprotinin has also been used in the treatment of septic shock, adult respiratory distress syndrome, acute pancreatitis, hemorrhagic shock, and other conditions (Westaby, Ann. Thorac. Surg.  
20 55:1033-1041, 1993; Wachtfogel et al., J. Thorac. Cardiovasc. Surg. 106:1-10, 1993). The clinical utility of aprotinin is believed to arise from its inhibitory activity towards plasma kallikrein or plasmin (Dennis et al., *ibid.*). Placental bikunin is a serine proteinase inhibitor containing two Kunitz domains (Delaria et al., J. Biol. Chem. 272:12209-12214, 1997). Individual Kunitz domains of bikunin have been expressed  
25 and shown to be potent inhibitors of trypsin, chymotrypsin, plasmin, factor XIa, and tissue and plasma kallikrein (Delaria et al., *ibid.*).

Known Kunitz-type inhibitors lack specificity and may have low potency. Lack of specificity can result in undesirable side effects, such as nephrotoxicity that occurs after repeated injections of high doses of aprotinin. These  
30 limitations may be overcome by preparing isolated Kunitz domains, which may have fewer side effects than traditional anticoagulants. Hence, there is a need in the art for additional Kunitz-type proteinase inhibitors.

#### BRIEF DESCRIPTION OF THE DRAWING

35 The attached drawing is a Hopp/Woods hydrophilicity profile of the zkun8 protein sequence shown in SEQ ID NO:2. The profile is based on a sliding six-

residue window. Buried G, S, and T residues and exposed H, Y, and W residues were ignored. These residues are indicated in the figure by lower case letters.

## DETAILED DESCRIPTION OF THE INVENTION

5 Prior to setting forth the invention in detail, it may be helpful to the understanding thereof to define the following terms:

The term "affinity tag" is used herein to denote a polypeptide segment that can be attached to a second polypeptide to provide for purification or detection of the second polypeptide or provide sites for attachment of the second polypeptide to a  
10 substrate. In principal, any peptide or protein for which an antibody or other specific binding agent is available can be used as an affinity tag. Affinity tags include a poly-histidine tract, protein A (Nilsson et al., EMBO J. 4:1075, 1985; Nilsson et al., Methods Enzymol. 198:3, 1991), glutathione S transferase (Smith and Johnson, Gene 67:31, 1988), Glu-Glu affinity tag (Glu-Tyr-Met-Pro-Met-Glu; SEQ ID NO:6) (Grussenmeyer  
15 et al., Proc. Natl. Acad. Sci. USA 82:7952-4, 1985), substance P, Flag™ peptide (Hopp et al., Biotechnology 6:1204-10, 1988), streptavidin binding peptide, or other antigenic epitope or binding domain. See, in general, Ford et al., Protein Expression and Purification 2: 95-107, 1991. DNAs encoding affinity tags are available from commercial suppliers (e.g., Pharmacia Biotech, Piscataway, NJ).

20 The term "allelic variant" is used herein to denote any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequence. The term allelic variant  
25 is also used herein to denote a protein encoded by an allelic variant of a gene.

The terms "amino-terminal" and "carboxyl-terminal" are used herein to denote positions within polypeptides. Where the context allows, these terms are used with reference to a particular sequence or portion of a polypeptide to denote proximity or relative position. For example, a certain sequence positioned carboxyl-terminal to a  
30 reference sequence within a polypeptide is located proximal to the carboxyl terminus of the reference sequence, but is not necessarily at the carboxyl terminus of the complete polypeptide.

A "complement" of a polynucleotide molecule is a polynucleotide molecule having a complementary base sequence and reverse orientation as compared  
35 to a reference sequence. For example, the sequence 5' ATGCA 3' is complementary to 5' CCCGT 3'.



The term "degenerate nucleotide sequence" denotes a sequence of nucleotides that includes one or more degenerate codons (as compared to a reference polynucleotide molecule that encodes a polypeptide). Degenerate codons contain different triplets of nucleotides, but encode the same amino acid residue (i.e., GAU and GAC triplets each encode Asp).

A "DNA segment" is a portion of a larger DNA molecule having specified attributes. For example, a DNA segment encoding a specified polypeptide is a portion of a longer DNA molecule, such as a plasmid or plasmid fragment, that, when read from the 5' to the 3' direction, encodes the sequence of amino acids of the specified polypeptide.

The term "expression vector" is used to denote a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of interest operably linked to additional segments that provide for its transcription. Such additional segments include promoter and terminator sequences, and may also include one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, etc. Expression vectors are generally derived from plasmid or viral DNA, or may contain elements of both.

The term "isolated", when applied to a polynucleotide, denotes that the polynucleotide has been removed from its natural genetic milieu and is thus free of other extraneous or unwanted coding sequences, and is in a form suitable for use within genetically engineered protein production systems. Such isolated molecules are those that are separated from their natural environment and include cDNA and genomic clones. Isolated DNA molecules of the present invention are free of other genes with which they are ordinarily associated, but may include naturally occurring 5' and 3' untranslated regions such as promoters and terminators. The identification of associated regions will be evident to one of ordinary skill in the art (see for example, Dynan and Tijan, *Nature* 316:774-78, 1985).

An "isolated" polypeptide or protein is a polypeptide or protein that is found in a condition other than its native environment, such as apart from blood and animal tissue. In a preferred form, the isolated polypeptide is substantially free of other polypeptides, particularly other polypeptides of animal origin. It is preferred to provide the polypeptides in a highly purified form, i.e. greater than 95% pure, more preferably greater than 99% pure. When used in this context, the term "isolated" does not exclude the presence of the same polypeptide in alternative physical forms, such as dimers or alternatively glycosylated or derivatized forms.

The term "operably linked", when referring to DNA segments, indicates that the segments are arranged so that they function in concert for their intended

purposes, e.g., transcription initiates in the promoter and proceeds through the coding segment to the terminator.

The term "ortholog" denotes a polypeptide or protein obtained from one species that is the functional counterpart of a polypeptide or protein from a different species. Sequence differences among orthologs are the result of speciation.

A "polynucleotide" is a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. Polynucleotides include RNA and DNA, and may be isolated from natural sources, synthesized *in vitro*, or prepared from a combination of natural and synthetic molecules. Sizes of polynucleotides are expressed as base pairs (abbreviated "bp"), nucleotides ("nt"), or kilobases ("kb"). Where the context allows, the latter two terms may describe polynucleotides that are single-stranded or double-stranded. When these terms are applied to double-stranded molecules they are used to denote overall length and will be understood to be equivalent to the term "base pairs". It will be recognized by those skilled in the art that the two strands of a double-stranded polynucleotide may differ slightly in length and that the ends thereof may be staggered as a result of enzymatic cleavage; thus all nucleotides within a double-stranded polynucleotide molecule may not be paired. Such unpaired ends will in general not exceed 20 nt in length.

A "polypeptide" is a polymer of amino acid residues joined by peptide bonds, whether produced naturally or synthetically. Polypeptides of less than about 10 amino acid residues are commonly referred to as "peptides".

The term "promoter" is used herein for its art-recognized meaning to denote a portion of a gene containing DNA sequences that provide for the binding of RNA polymerase and initiation of transcription. Promoter sequences are commonly, but not always, found in the 5' non-coding regions of genes.

A "protein" is a macromolecule comprising one or more polypeptide chains. A protein may also comprise non-peptidic components, such as carbohydrate groups. Carbohydrates and other non-peptidic substituents may be added to a protein by the cell in which the protein is produced, and will vary with the type of cell. Proteins are defined herein in terms of their amino acid backbone structures; substituents such as carbohydrate groups are generally not specified, but may be present nonetheless.

The term "secretory signal sequence" denotes a DNA sequence that encodes a polypeptide (a "secretory peptide") that, as a component of a larger polypeptide, directs the larger polypeptide through a secretory pathway of a cell in which it is synthesized. The larger polypeptide is commonly cleaved to remove the secretory peptide during transit through the secretory pathway.

The term "splice variant" is used herein to denote alternative forms of RNA transcribed from a gene. Splice variation arises naturally through use of alternative splicing sites within a transcribed RNA molecule, or less commonly between separately transcribed RNA molecules, and may result in several mRNAs transcribed from the same gene. Splice variants may encode polypeptides having altered amino acid sequence. The term splice variant is also used herein to denote a protein encoded by a splice variant of an mRNA transcribed from a gene.

Molecular weights and lengths of polymers determined by imprecise analytical methods (e.g., gel electrophoresis) will be understood to be approximate values. When such a value is expressed as "about" X or "approximately" X, the stated value of X will be understood to be accurate to  $\pm 10\%$ .

All references cited herein are incorporated by reference in their entirety.

The present invention provides, in part, novel serine proteinases comprising at least one Kunitz domain. Also included are polypeptides comprising a first and second kunitz domain and can further comprise a C-terminal domain. The molecule containing one or more kunitz domains, including sequence variants thereof and proteins containing it, is referred to herein as "zkun8". The zkun8 polypeptide sequence shown in SEQ ID NO:2 comprises a first Kunitz domain, which is bounded at the amino and carboxyl termini by residues at positions 324 (Pro) and 381 (Gly), and a second kunitz domain, which is bounded at the amino and carboxyl termini by residues at positions 382 (Pro) and 440 (Arg), respectively. The corresponding nucleotide sequences encoding for the kunitz domains described herein are shown in SEQ ID NO: 1.

In other embodiments, the molecule of the present invention comprises a first and/or second kunitz domain followed by a cysteine-rich C-terminal domain, which bounded at the amino and carboxyl termini by residues 441 (Gly) and 576 (His) as shown in SEQ ID NO: 2, with corresponding nucleotide sequence shown in SEQ ID NO: 1. Another embodiment includes a molecule comprising a first and/or second kunitz domain preceded by an N-terminus secretory signal sequence. An exemplary secretory signal sequence is the sequence as shown in SEQ ID NO: 2 from amino acid residue 1 (Met) to amino acid residue 34 (Ala), with the corresponding nucleotide sequence shown in SEQ ID NO: 1. Additional embodiments include an N-terminal sequence as shown in SEQ ID NO: 2 from amino acid residue 1 (Met) to amino acid residue 323 (Phe), with corresponding nucleotide sequence encoding for said amino acids shown in SEQ ID NO: 1.

The first kunitz domain of Zkun8 has 32% amino acid residue identity with the kunitz domain in beta-1 bungarotoxin B chain (Kondo et al., *J. Biochem.*

83:101-115, 1978), and the second kunitz domain of zkun8 has 49% amino acid residue identity to the kunitz domain in human alpha-1-microglobulin-bikunin (Vetr et al., Biol. Chem. Hoppe Seyler 371:1185-1196, 1990). The structure of the 51-residue kunitz domain in human alpha-3-type-VI collagen domain has been solved by X-ray crystallography and by NMR (Arnoux et al., J. Mol. Biol. 246:609-617, 1995; Sorensen et al., Biochemistry 36:10439-10450, 1997). An alignment of kunitz domains of zkun8 and the collagen Kunitz domain, in combination with the X-ray structure of collagen, may be used to predict the function of certain residues in zkun8. Referring to SEQ ID NO:2, disulfide bonds are predicted to be formed by paired cysteine residues Cys328 – Cys378; Cys337 – Cys361; Cys353 – Cys374; Cys386 – Cys436; Cys395 – Cys419; and Cys411 – Cys432. In the first kunitz domain, protease binding loop (P3-P4') is expected to comprise residues 336-346 of SEQ ID NO:2, with the P1 residue being Gly338. In the second kunitz domain, the protease binding loop (P3-P4') is expected to comprise residues 382-400 of SEQ ID NO: 2, with the P1 residue being Lys396.

The secretory signal sequence of zkun8 comprises amino acid residues 1-34 of SEQ ID NO: 2. However, certain polypeptides with potential secretion signal sequences are not cleaved by signal peptidase and remain bound to membrane require a cleavage as part of the activation process. Generally, cleavage is proteolytic and can occur, for example at a dibasic site such as ArgArg, LysArg, ArgLys, or LysLys, or even at a single basic amino acid residue. Other domains found in zkun8 include, a four-disulfide core proteinase inhibitor as shown in amino acid residues 35-98, with a minimum structure found within this domain located at amino acid residues 45-88 of SEQ ID NO: 2; a follistatin-type proteinase inhibitor domain as shown in amino acid residues 101-180, with a minimum structure found within this domain located at amino acid residues 111-175 of SEQ ID NO: 2; and an I-set IG domain as shown in SEQ ID NO: 2 from amino acid residues 227-378. The corresponding nucleotide sequence that encodes for these domains is shown in SEQ ID NO: 1.

The "four-disulfide core" or Chelonianin type serine proteinase inhibitor domain family, as shown in amino acid residues 35-98, is characterized by a common structural motif which comprises two adjacent beta-hairpin motifs, each consisting of two antiparallel beta strands connected by a loop region. The secondary structure of this motif is depicted by beta-sheet topology K (Branden and Tooze, *Introduction to Protein Structure*, Garland Publishing, Inc., 1991). The beta strands are linked by intra-chain hydrogen bonding and by a network of four disulfide bonds. These disulfide bonds stabilize the structure of the proteinase inhibitor and render it less susceptible to degradation. This structural feature has caused the Chelonianin family to be referred to as the "four-disulfide core" family of proteinase inhibitors. The family includes human

antileukoproteinase, human elafin, guinea pig caltrin-like protein, human kallman syndrome protein, sea turtle chelonianin, the mouse WDNM1 protein, and human epididymal secretory protein E4, and trout TOP-2, and *C. Elegans* C08G9. Several of these family members contain several copies of this structural motif.

5           The domain, located at amino acid residues 111-175 of SEQ ID NO: 2, has homology to a follistatin homology in SPARC (Swiss-Prot SPRC\_HUMAN, PDB 1BMO, also known as BM-40 or osteonectin) (Hohenester et al. EMBO 16(13):3778-86 1997). This is a beta hairpin structure, followed by a small hydrophobic core of alpha/beta structure. The follistatin homology domain has substantial sequence  
10 similarity to the Kazal family (Bode and Huber, Eur. J. Biochem., 204, 433-451 1992) of serine proteinase inhibitors.

          The I-set IG domain, as shown in SEQ ID NO: 2 from amino acid residues 227-378, is predicted to fold into a structure similar to that determined for the telokin peptide (Swiss-Prot KMLS\_HUMAN, PDB 1TLK). The telokin peptide falls  
15 into the class of immunoglobulins (Bork et al., J. Mol. Biol. 242:309-320 1994) which are all beta proteins folding into a beta-sandwich like structure. These have two beta sheets comprising 3+4 beta strands. Furthermore, the telokin peptide has been subclassified as an "I" set immunoglobulin domain. Other proteins with I set immunoglobulin domains include titin, vascular and neural cell adhesion molecules,  
20 and twitchin.

          The C-terminus of zkun8 (amino acid residues 441-576 of SEQ ID NO:2) appears to have homology with the Domain C of the netrin family. Netrins have been associated with axon outgrowth (Serafini et al., Cell 78:409-424, 1994). Domain C, which is found at the C-terminus of the netrins, is rich in basic amino acid residues  
25 on the C-terminus. This basic amino acid rich region is characteristic of heparin binding domains and similar sequences of netrin have been implicated in heparin binding. Fibroblast growth factors contain a heparin binding domain as well, and it is postulated that receptor-mediated signaling is initiated upon binding of FGF ligand complexed with cell-surface heparin sulfate proteoglycans. The putative heparin  
30 binding domain in zkun8 may play a similar function, i.e., complexing with some molecule that associates with the cell surface or membrane.

          The formation of complexes between two or more different molecules to inhibit proteolytic activation is seen, for example, in the formation of a quaternary complex of Factor Xa (Xa)-Tissue Factor (TF)-Factor VIIa (VIIa)-Tissue Factor  
35 Pathway Inhibitor (TFPI). In the Xa-TF-VIIa-TFPI complex TFPI comprises three kunitz domains followed by a C-terminal basic region, of which K1 and K2 are believed to bind VIIa and Xa, respectively (Broze et al., Biochem. 29:7539-7546,

1990). In addition, heparin has been shown to enhance binding of the target molecules to TFPI (*Ibid.* at 7541). Therefore, it is possible that zkun8 inhibits proteolysis by forming a complex, with each of the two kunitz domains and the C-terminal basic region interacting with separate molecules. The different amino acid residues at the P1 position for the first kunitz domain and the second kunitz domain lend further support to this hypothesis.

Amino acid substitutions can be made within the zkun8 sequence so long as the conserved cysteine residues are retained and the higher order structure is not disrupted. It is preferred to make substitutions within the zkun8 Kunitz domain by reference to the sequences of other Kunitz domains. SEQ ID NO:7 is a generalized Kunitz domain sequence that shows allowable amino acid substitutions based on such an alignment. However, mutants can be made that would purposely alter binding specificity and inhibition profiles. The 51-residue sequence shown in SEQ ID NO:7 conforms to the pattern:

C-X(8)-C-X(15)-C-X(7)-C-X(12)-C-X(3)-C

wherein C denotes cysteine; X is any naturally occurring amino acid residue. SEQ ID NO: 4 is the kunitz motif for the first kunitz domain of zkun8, corresponding to residues 328-378 of SEQ ID NO: 2. Therefore, substitutions of the first kunitz domain of zkun8 are subject to the limitations set forth in the attached Sequence Listing for SEQ ID NO:4; and the numerals indicate the number of such variable residues. SEQ ID NO: 5 is the kunitz motif for the second kunitz domain of zkun8, corresponding to residues 386-436 of SEQ ID NO: 2. Therefore, substitutions of the second kunitz domain of zkun8 are subject to the limitations set forth in the attached Sequence Listing for SEQ ID NO:5; and the numerals indicate the number of such variable residues.

Within the present invention up to 20% of the amino acid residues in the zkun8 Kunitz domains (residues 328 through 378 and residues 386 through 436 of SEQ ID NO:2) can be replaced with other amino acid residues, subject to the limitation that the resulting substituted sequence is one of the sequences disclosed in SEQ ID NO:4 or SEQ ID NO: 5, respectively. In one embodiment, the present invention thus provides a family of proteins comprising a sequence of amino acid residues that is at least 80% identical to residues 328 through 378 as shown in SEQ ID NO:2, wherein any variation of residues is subject to the limitations as shown in SEQ ID NO: 4. In another embodiment, the present invention provides a family of proteins comprising a sequence of amino acid residues that is at least 80% identical to residues 386 through 436 as shown in SEQ ID NO:2, wherein any variation of residues is subject to the limitations as shown in SEQ ID NO: 4. In other embodiments of the present invention, the proteins of the present invention comprise such a sequence that is at least 85%, at least

90%, and at least 95%, 96%, 97%, 98% or 99% identical to residues 328 through 378 as shown in SEQ ID NO:2, wherein any variation of residues is subject to the limitations as shown in SEQ ID NO: 4. In another embodiment, the present invention provides a family of proteins comprising a sequence of amino acid residues that is at least 85%, at least 90%, and at least 95%, 96%, 97%, 98% or 99% identical to residues 386 through 436 as shown in SEQ ID NO:2, wherein any variation of residues is subject to the limitations as shown in SEQ ID NO: 5.

Percent sequence identity is determined by conventional methods. See, for example, Altschul et al., *Bull. Math. Bio.* 48:603-616, 1986, and Henikoff and Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915-10919, 1992. Briefly, two amino acid sequences are aligned to optimize the alignment scores using a gap opening penalty of 10, a gap extension penalty of 1, and the "BLOSUM62" scoring matrix of Henikoff and Henikoff (*ibid.*) as shown in Table 1 (amino acids are indicated by the standard one-letter codes). The percent identity is then calculated as:

15

Total number of identical matches

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x 100

[length of the longer sequence plus the  
number of gaps introduced into the longer  
sequence in order to align the two sequences]

20

Table 1

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	4																			
R	-1	5																		
N	-2	0	6																	
D	-2	-2	1	6																
C	0	-3	-3	-3	9															
Q	-1	1	0	0	-3	5														
E	-1	0	0	2	-4	2	5													
G	0	-2	0	-1	-3	-2	-2	6												
H	-2	0	1	-1	-3	0	0	-2	8											
I	-1	-3	-3	-3	-1	-3	-3	-4	-3	4										
L	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4									
K	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5								
M	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	5							
F	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6						
P	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7					
S	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4				
T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5			
W	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11		
Y	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	
V	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4

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The level of identity between amino acid sequences can be determined using the "FASTA" similarity search algorithm disclosed by Pearson and Lipman (Proc. Natl. Acad. Sci. USA 85:2444, 1988) and by Pearson (Meth. Enzymol. 183:63, 1990). Briefly, FASTA first characterizes sequence similarity by identifying regions shared by the query sequence (e.g., SEQ ID NO:2) and a test sequence that have either the highest density of identities (if the ktup variable is 1) or pairs of identities (if ktup=2), without considering conservative amino acid substitutions, insertions, or deletions. The ten regions with the highest density of identities are then rescored by comparing the similarity of all paired amino acids using an amino acid substitution matrix, and the ends of the regions are "trimmed" to include only those residues that contribute to the highest score. If there are several regions with scores greater than the "cutoff" value (calculated by a predetermined formula based upon the length of the sequence and the ktup value), then the trimmed initial regions are examined to determine whether the regions can be joined to form an approximate alignment with gaps. Finally, the highest scoring regions of the two amino acid sequences are aligned using a modification of the Needleman-Wunsch-Sellers algorithm (Needleman and Wunsch, J. Mol. Biol. 48:444, 1970; Sellers, SIAM J. Appl. Math. 26:787, 1974), which allows for amino acid insertions and deletions. Preferred parameters for FASTA analysis are: ktup=1, gap opening penalty=10, gap extension penalty=1, and substitution matrix=BLOSUM62. These parameters can be introduced into a FASTA program by modifying the scoring matrix file ("SMATRIX"), as explained in Appendix 2 of Pearson, 1990 (*ibid.*).

FASTA can also be used to determine the sequence identity of nucleic acid molecules using a ratio as disclosed above. For nucleotide sequence comparisons, the ktup value can range between one to six, preferably from three to six, most preferably three, with other parameters set as default.

The proteins of the present invention can also comprise non-naturally occurring amino acid residues. Non-naturally occurring amino acids include, without limitation, *trans*-3-methylproline, 2,4-methanoproline, *cis*-4-hydroxyproline, *trans*-4-hydroxyproline, *N*-methylglycine, *allo*-threonine, methylthreonine, hydroxyethylcysteine, hydroxyethylhomocysteine, nitroglutamine, homoglutamine, pipercolic acid, thiazolidine carboxylic acid, dehydroproline, 3- and 4-methylproline, 3,3-dimethylproline, *tert*-leucine, norvaline, 2-azaphenylalanine, 3-azaphenylalanine, 4-azaphenylalanine, and 4-fluorophenylalanine. Several methods are known in the art for incorporating non-naturally occurring amino acid residues into proteins. For example, an *in vitro* system can be employed wherein nonsense mutations are suppressed using chemically aminoacylated suppressor tRNAs. Methods for synthesizing amino acids and aminoacylating tRNA are known in the art. Transcription and translation of

plasmids containing nonsense mutations is carried out in a cell-free system comprising an *E. coli* S30 extract and commercially available enzymes and other reagents. Proteins are purified by chromatography. See, for example, Robertson et al., J. Am. Chem. Soc. 113:2722, 1991; Ellman et al., Methods Enzymol. 202:301, 1991; Chung et al., Science 259:806-9, 1993; and Chung et al., Proc. Natl. Acad. Sci. USA 90:10145-9, 1993). In a second method, translation is carried out in *Xenopus* oocytes by microinjection of mutated mRNA and chemically aminoacylated suppressor tRNAs (Turcatti et al., J. Biol. Chem. 271:19991-8, 1996). Within a third method, *E. coli* cells are cultured in the absence of a natural amino acid that is to be replaced (e.g., phenylalanine) and in the presence of the desired non-naturally occurring amino acid(s) (e.g., 2-azaphenylalanine, 3-azaphenylalanine, 4-azaphenylalanine, or 4-fluorophenylalanine). The non-naturally occurring amino acid is incorporated into the protein in place of its natural counterpart. See, Koide et al., Biochem. 33:7470-6, 1994. Naturally occurring amino acid residues can be converted to non-naturally occurring species by *in vitro* chemical modification. Chemical modification can be combined with site-directed mutagenesis to further expand the range of substitutions (Wynn and Richards, Protein Sci. 2:395-403, 1993).

Amino acid sequence changes described herein are made in *zkun8* polypeptides so as to minimize disruption of higher order structure essential to biological activity. Amino acid residues that are critical to maintaining structural integrity can be determined. As shown in SEQ ID NO: 4 specific residues that will be more or less tolerant of change and maintain the overall tertiary structure of the molecule have been described. Methods for analyzing sequence structure include, but are not limited to, alignment of multiple sequences with high amino acid or nucleotide identity, secondary structure propensities, binary patterns, complementary packing, and buried polar interactions (Barton, Current Opin. Struct. Biol. 5:372-376, 1995 and Cordes et al., Current Opin. Struct. Biol. 6:3-10, 1996). In general, determination of structure will be accompanied by evaluation of activity of modified molecules. For example, changes in amino acid residues will be made so as not to disrupt the protease binding loop structure of the protein family. The effects of amino acid sequence changes can be predicted by, for example, computer modeling using available software (e.g., the Insight II® viewer and homology modeling tools; MSI, San Diego, CA) or determined by analysis of crystal structure (see, e.g., Laphorn et al., Nature 369:455-461, 1994; Laphorn et al., Nat. Struct. Biol. 2:266-268, 1995). Protein folding can be measured by circular dichroism (CD). Measuring and comparing the CD spectra generated by a modified molecule and standard molecule are routine in the art (Johnson, Proteins 7:205-214, 1990). Crystallography is another well known and accepted method for analyzing folding and structure. Nuclear magnetic resonance

(NMR), digestive peptide mapping and epitope mapping are other known methods for analyzing folding and structural similarities between proteins and polypeptides (Schaanan et al., Science 257:961-964, 1992). Mass spectrometry and chemical modification using reduction and alkylation can be used to identify cysteine residues that are associated with disulfide bonds or are free of such associations (Bean et al., Anal. Biochem. 201:216-226, 1992; Gray, Protein Sci. 2:1732-1748, 1993; and Patterson et al., Anal. Chem. 66:3727-3732, 1994). Alterations in disulfide bonding will be expected to affect protein folding. These techniques can be employed individually or in combination to analyze and compare the structural features that affect folding of a variant protein or polypeptide to a standard molecule to determine whether such modifications would be significant.

Essential amino acids in the polypeptides of the present invention can be identified experimentally according to procedures known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, Science 244, 1081-1085, 1989; Bass et al., Proc. Natl. Acad. Sci. USA 88:4498-4502, 1991). In the latter technique, single alanine mutations are introduced at every residue in the molecule, and the resultant mutant molecules are tested for biological activity as disclosed below to identify amino acid residues that are critical to the activity of the molecule.

Multiple amino acid substitutions can be made and tested using known methods of mutagenesis and screening, such as those disclosed by Reidhaar-Olson and Sauer (Science 241:53-57, 1988) or Bowie and Sauer (Proc. Natl. Acad. Sci. USA 86:2152-2156, 1989). Briefly, these authors disclose methods for simultaneously randomizing two or more positions in a polypeptide, selecting for functional polypeptide, and then sequencing the mutagenized polypeptides to determine the spectrum of allowable substitutions at each position. Other methods that can be used include phage display (e.g., Lowman et al., Biochem. 30:10832-10837, 1991; Ladner et al., U.S. Patent No. 5,223,409; Huse, WIPO Publication WO 92/06204) and region-directed mutagenesis (Derbyshire et al., Gene 46:145, 1986; Ner et al., DNA 7:127, 1988).

Variants of the disclosed zkun8 DNA and polypeptide sequences can be generated through DNA shuffling as disclosed by Stemmer, Nature 370:389-391, 1994 and Stemmer, Proc. Natl. Acad. Sci. USA 91:10747-10751, 1994. Briefly, variant genes are generated by *in vitro* homologous recombination by random fragmentation of a parent gene followed by reassembly using PCR, resulting in randomly introduced point mutations. This technique can be modified by using a family of parent genes, such as allelic variants or genes from different species, to introduce additional

variability into the process. Selection or screening for the desired activity, followed by additional iterations of mutagenesis and assay provides for rapid "evolution" of sequences by selecting for desirable mutations while simultaneously selecting against detrimental changes.

5 In many cases, the structure of the final polypeptide product will result from processing of the nascent polypeptide chain by the host cell, thus the final sequence of a zkun8 polypeptide produced by a host cell will not always correspond to the full sequence encoded by the expressed polynucleotide. For example, expressing the complete zkun8 sequence in a cultured mammalian cell is expected to result in  
10 removal of at least the secretory peptide, while the same polypeptide produced in a prokaryotic host would not be expected to be cleaved. Differential processing of individual chains may result in heterogeneity of expressed polypeptides.

Additional polypeptides may be joined to the amino and/or carboxyl termini of the zkun8 Kunitz domains (residues 324-381, for the first kunitz domain; and  
15 residues 382-440 for the second kunitz domain of SEQ ID NO:2, respectively), a derivative of the zkun8 Kunitz domains, or other zkun8 domains and their derivatives, as disclosed above. Amino and carboxyl extensions of the zkun8 Kunitz domains will be selected so as not to destroy or mask the proteinase-inhibiting activity of the protein by, for example, burying the Kunitz domains within the interior of the protein. There is  
20 a consequent preference for shorter extensions, typically 10-15 residues in length, preferably not exceeding 8 residues in length. There is considerable latitude in the permissible sequence of these extensions, although it is preferred to avoid the addition of cysteine residues in close proximity to the Kunitz domain itself. For example, a zkun8 protein can comprise residues 324-381, for the first kunitz domain; and residues  
25 382-440 for the second kunitz domain of SEQ ID NO:2, respectively, with amino- and carboxyl-terminal dipeptides, wherein the individual amino acid residues of the dipeptides are any amino acid residue except cysteine.

Other amino- and carboxyl-terminal extensions that can be included in the proteins of the present invention include, for example, an amino-terminal  
30 methionine residue, a small linker peptide of up to about 20-25 residues, or an affinity tag as disclosed above. A protein comprising such an extension may further comprise a polypeptide linker and/or a proteolytic cleavage site between the zkun8 portion and the affinity tag. Preferred cleavage sites include thrombin cleavage sites and factor Xa cleavage sites. For example, a zkun8 polypeptide of 50 amino acid residues can be  
35 expressed as a fusion comprising, from amino terminus to carboxyl terminus: maltose binding protein (approximately 370 residues)--polyhistidine (6 residues)--thrombin cleavage site--zkun8. In a second example, a zkun8 polypeptide of 50 residues can be

fused to *E. coli*  $\beta$ -galactosidase (1,021 residues; see Casadaban et al., J. Bacteriol. 143:971-980, 1980), a 10-residue spacer, and a 4-residue factor Xa cleavage site. Linker peptides and affinity tags provide for additional functions, such as binding to substrates, antibodies, binding proteins, and the like, and facilitate purification, detection, and delivery of zkun8 proteins. In another example, a zkun8 Kunitz domain can be expressed as a secreted protein comprising a carboxyl-terminal receptor transmembrane domain, permitting the Kunitz domain to be displayed on the surface of a cell. To span the lipid bilayer of the cell membrane, a minimum of about 20 amino acids are required in the transmembrane domain; these should predominantly be hydrophobic amino acids. The Kunitz domain can be separated from the transmembrane domain by a spacer polypeptide, and can be contained within an extended polypeptide comprising a carboxyl-terminal transmembrane domain-spacer polypeptide-Kunitz domain-amino-terminal polypeptide. Many receptor transmembrane domains and polynucleotides encoding them are known in the art. The spacer polypeptide will generally be at least about 50 amino acid residues in length, up to 200-300 or more residues. The amino terminal polypeptide may be up to 300 or more residues in length.

The present invention also provides polypeptide fragments or peptides comprising an epitope-bearing portion of a zkun8 polypeptide described herein. Such fragments or peptides may comprise an "immunogenic epitope," which is a part of a protein that elicits an antibody response when the entire protein is used as an immunogen. Immunogenic epitope-bearing peptides can be identified using standard methods (see, for example, Geysen *et al.*, Proc. Nat'l Acad. Sci. USA 81:3998 (1983)).

In contrast, polypeptide fragments or peptides may comprise an "antigenic epitope," which is a region of a protein molecule to which an antibody can specifically bind. Certain epitopes consist of a linear or contiguous stretch of amino acids, and the antigenicity of such an epitope is not disrupted by denaturing agents. It is known in the art that relatively short synthetic peptides that can mimic epitopes of a protein can be used to stimulate the production of antibodies against the protein (see, for example, Sutcliffe *et al.*, Science 219:660 (1983)). Antibodies that recognize short linear epitopes are particularly useful in analytic and diagnostic applications that use denatured protein, such as Western analysis, or in the analysis of fixed cells or tissue samples. Antibodies to linear epitopes are also useful for detecting fragments of zkun8, such as might occur in body fluids or culture media. Accordingly, antigenic epitope-bearing peptides and polypeptides of the present invention are useful to raise antibodies that bind with the polypeptides described herein.

Antigenic epitope-bearing peptides and polypeptides can contain at least four to ten amino acids, at least ten to fifteen amino acids, or about 15 to about 30 amino acids of SEQ ID NO:2. Such epitope-bearing peptides and polypeptides can be produced by fragmenting a zkun8 polypeptide, or by chemical peptide synthesis, as described herein. Moreover, epitopes can be selected by phage display of random peptide libraries (see, for example, Lane and Stephen, Curr. Opin. Immunol. 5:268 (1993), and Cortese *et al.*, Curr. Opin. Biotechnol. 7:616 (1996)). Standard methods for identifying epitopes and producing antibodies from small peptides that comprise an epitope are described, for example, by Mole, "Epitope Mapping," in *Methods in Molecular Biology*, Vol. 10, Manson (ed.), pages 105-116 (The Humana Press, Inc. 1992), Price, "Production and Characterization of Synthetic Peptide-Derived Antibodies," in *Monoclonal Antibodies: Production, Engineering, and Clinical Application*, Ritter and Ladyman (eds.), pages 60-84 (Cambridge University Press 1995), and Coligan *et al.* (eds.), *Current Protocols in Immunology*, pages 9.3.1 - 9.3.5 and pages 9.4.1 - 9.4.11 (John Wiley & Sons 1997).

The present invention provides a series of hybrid molecules in which a segment comprising one or more of the domains of zkun8 is fused to another polypeptide. Fusion is preferably done by splicing at the DNA level to allow expression of chimeric molecules in recombinant production systems. The resultant molecules are then assayed for such properties as improved solubility, improved stability, prolonged clearance half-life, improved expression and secretion levels, and pharmacodynamics. Such hybrid molecules may further comprise additional amino acid residues (e.g. a polypeptide linker) between the component proteins or polypeptides. The present invention further provides a variety of other polypeptide fusions (and related multimeric proteins comprising one or more polypeptide fusions). For example, a zkun8 polypeptide can be prepared as a fusion to a dimerizing protein as disclosed in U.S. Patents Nos. 5,155,027 and 5,567,584. Preferred dimerizing proteins in this regard include immunoglobulin constant region domains. Immunoglobulin-zkun8 polypeptide fusions can be expressed in genetically engineered cells (to produce a variety of multimeric zkun8 analogs). Auxiliary domains can be fused to zkun8 polypeptides to target them to specific cells, tissues, or macromolecules. For example, a zkun8 polypeptide or protein could be targeted to a predetermined cell type by fusing a zkun8 polypeptide to a ligand that specifically binds to a receptor on the surface of that target cell. In this way, polypeptides and proteins can be targeted for therapeutic or diagnostic purposes. A zkun8 polypeptide can be fused to two or more moieties, such as an affinity tag for purification and a targeting domain. Polypeptide fusions can

also comprise one or more cleavage sites, particularly between domains. See, Tuan et al., Connective Tissue Research 34:1-9, 1996.

Fusion proteins can be prepared by methods known to those skilled in the art by preparing each component of the fusion protein and chemically conjugating them. Alternatively, a polynucleotide encoding both components of the fusion protein in the proper reading frame can be generated using known techniques and expressed by the methods described herein. For example, part or all of a collagen or Kunitz conferring a biological function may be swapped between zkun8 of the present invention with the functionally equivalent domains from another family member, such as Type 6 collagen, TFPI or TFPI-2. Such components include, but are not limited to, the secretory signal sequence; globular domains, Kunitz domains, helical domains, and von Willebrand domains. Such fusion proteins would be expected to have a biological functional profile that is the same or similar to polypeptides of the present invention or other known serine protease inhibitor family proteins, depending on the fusion constructed. Moreover, such fusion proteins may exhibit other properties as disclosed herein.

Standard molecular biological and cloning techniques can be used to swap the equivalent domains between the zkun8 polypeptide and those polypeptides to which they are fused. Generally, a DNA segment that encodes a domain of interest, e.g., zkun8 Kunitz, or other domains described herein, is operably linked in frame to at least one other DNA segment encoding an additional polypeptide, and inserted into an appropriate expression vector, as described herein. Generally DNA constructs are made such that the several DNA segments that encode the corresponding regions of a polypeptide are operably linked in frame to make a single construct that encodes the entire fusion protein, or a functional portion thereof. For example, a DNA construct would encode from N-terminus to C-terminus a fusion protein comprising a signal polypeptide followed by a collagen domain fusion protein containing one or more von Willebrand domains, followed by one or more Kunitz domains. Such fusion proteins can be expressed, isolated, and assayed for activity as described herein.

Also disclosed herein are polynucleotide molecules, including DNA and RNA molecules, encoding zkun8 proteins. These polynucleotides include the sense strand; the anti-sense strand; and the DNA as double-stranded, having both the sense and anti-sense strand annealed together by their respective hydrogen bonds. A representative DNA sequence encoding a zkun8 protein is set forth in SEQ ID NO:1. DNA sequences encoding other zkun8 proteins can be readily generated by those of ordinary skill in the art based on the genetic code. Counterpart RNA sequences can be generated by substitution of U for T. Polynucleotides encoding zkun8 proteins and

complementary polynucleotides are useful in the production of zkun8 proteins and for diagnostic and investigatory purposes.

Those skilled in the art will readily recognize that, in view of the degeneracy of the genetic code, considerable sequence variation is possible among these polynucleotide molecules. SEQ ID NO:3 is a degenerate DNA sequence that encompasses all DNAs that encode the zkun8 polypeptide of SEQ ID NO:2. Those skilled in the art will recognize that the degenerate sequence of SEQ ID NO:3 also provides all RNA sequences encoding SEQ ID NO:2 by substituting U for T. Thus, zkun8 polypeptide-encoding polynucleotides comprising nucleotide 1 to nucleotide 1728 of SEQ ID NO:3 and their respective RNA equivalents are contemplated by the present invention. Table 2 sets forth the one-letter codes used within SEQ ID NO:3 to denote degenerate nucleotide positions. "Resolutions" are the nucleotides denoted by a code letter. "Complement" indicates the code for the complementary nucleotide(s). For example, the code Y denotes either C or T, and its complement R denotes A or G, A being complementary to T; and G being complementary to C.



TABLE 2

Nucleotide	Resolution	Nucleotide	Complement
A	A	T	T
C	C	G	G
G	G	C	C
T	T	A	A
R	A G	Y	C T
Y	C T	R	A G
M	A C	K	G T
K	G T	M	A C
S	C G	S	C G
W	A T	W	A T
H	A C T	D	A G T
B	C G T	V	A C G
V	A C G	B	C G T
D	A G T	H	A C T
N	A C G T	N	A C G T

The degenerate codons used in SEQ ID NO:3, encompassing all possible  
5 codons for a given amino acid, are set forth in Table 3.

TABLE 3

Amino Acid	One Letter Code	Codons	Degenerate Codon
Cys	C	TGC TGT	TGY
Ser	S	AGC AGT TCA TCC TCG TCT	WSN
Thr	T	ACA ACC ACG ACT	ACN
Pro	P	CCA CCC CCG CCT	CCN
Ala	A	GCA GCC GCG GCT	GCN
Gly	G	GGA GGC GGG GGT	GGN
Asn	N	AAC AAT	AAY
Asp	D	GAC GAT	GAY
Glu	E	GAA GAG	GAR
Gln	Q	CAA CAG	CAR
His	H	CAC CAT	CAY
Arg	R	AGA AGG CGA CGC CGG CGT	MGN
Lys	K	AAA AAG	AAR
Met	M	ATG	ATG
Ile	I	ATA ATC ATT	ATH
Leu	L	CTA CTC CTG CTT TTA TTG	YTN
Val	V	GTA GTC GTG GTT	GTN
Phe	F	TTC TTT	TTY
Tyr	Y	TAC TAT	TAY
Trp	W	TGG	TGG
Ter	.	TAA TAG TGA	TRR
Asn Asp	B		RAY
Glu Gln	Z		SAR
Any	X		NNN

One of ordinary skill in the art will appreciate that some ambiguity is introduced in determining a degenerate codon, representative of all possible codons encoding each amino acid. For example, the degenerate codon for serine (WSN) can, in some circumstances, encode arginine (AGR), and the degenerate codon for arginine (MGN) can, in some circumstances, encode serine (AGY). A similar relationship exists between codons encoding phenylalanine and leucine. Thus, some polynucleotides encompassed by the degenerate sequence may encode variant amino acid sequences, but one of ordinary skill in the art can easily identify such variant sequences by reference to the amino acid sequences shown in SEQ ID NO:2. Variant sequences can be readily tested for functionality as described herein.

One of ordinary skill in the art will also appreciate that different species can exhibit preferential codon usage. See, in general, Grantham et al., Nuc. Acids Res. 8:1893-912, 1980; Haas et al. Curr. Biol. 6:315-24, 1996; Wain-Hobson et al., Gene 13:355-64, 1981; Grosjean and Fiers, Gene 18:199-209, 1982; Holm, Nuc. Acids Res. 14:3075-87, 1986; and Ikemura, J. Mol. Biol. 158:573-97, 1982. "Preferential codon usage" is a term of art referring to the bias in codon usage within the genomes of certain species, whereby certain protein translation codons are more frequently used, thus favoring one or a few representatives of the possible codons encoding each amino acid (see Table 3). For example, the amino acid threonine (Thr) may be encoded by ACA, ACC, ACG, or ACT, but in mammalian cells ACC is the most commonly used codon. In other species, for example, insect cells, yeast, viruses or bacteria, different Thr codons may be preferred. Preferred codons for a particular species can be introduced into the polynucleotides of the present invention by a variety of methods known in the art. Introduction of preferred codon sequences into recombinant DNA can, for example, enhance production of the protein by making protein translation more efficient within a particular cell type or species. Therefore, the degenerate codon sequence disclosed in SEQ ID NO: 3 serves as a template for optimizing expression of polynucleotides in various cell types and species commonly used in the art and disclosed herein. Sequences containing preferred codons can be tested and optimized for expression in various host cell species, and tested for functionality as disclosed herein.

Within certain embodiments of the invention the isolated polynucleotides will hybridize to similar sized regions of SEQ ID NO:1 or a sequence complementary thereto under stringent conditions. In general, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly

matched probe. Typical stringent conditions are those in which the salt concentration is up to about 0.03 M at pH 7 and the temperature is at least about 60°C.

As previously noted, the isolated polynucleotides of the present invention include DNA and RNA. Methods for preparing DNA and RNA are well known in the art. In general, RNA is isolated from a tissue or cell that produces large amounts of zkun8 RNA. Total RNA can be prepared using guanidine HCl extraction followed by isolation by centrifugation in a CsCl gradient (Chirgwin et al., Biochemistry 18:52-94, 1979). Poly (A)<sup>+</sup> RNA is prepared from total RNA using the method of Aviv and Leder (Proc. Natl. Acad. Sci. USA 69:1408-1412, 1972). Complementary DNA (cDNA) is prepared from poly(A)<sup>+</sup> RNA using known methods. In the alternative, genomic DNA can be isolated. Polynucleotides encoding zkun8 polypeptides are then identified and isolated by, for example, hybridization or PCR.

Full-length clones encoding zkun8 can be obtained by conventional cloning procedures. Complementary DNA (cDNA) clones are preferred, although for some applications (e.g., expression in transgenic animals) it may be preferable to use a genomic clone, or to modify a cDNA clone to include at least one genomic intron. Methods for preparing cDNA and genomic clones are well known and within the level of ordinary skill in the art, and include the use of the sequence disclosed herein, or parts thereof, for probing or priming a library. Expression libraries can be probed with antibodies to zkun8, receptor fragments, or other specific binding partners.

Zkun8 polynucleotide sequences disclosed herein can also be used as probes or primers to clone 5' non-coding regions of a zkun8 gene. Promoter elements from a zkun8 gene can thus be used to direct the expression of heterologous genes in, for example, transgenic animals or patients treated with gene therapy. Cloning of 5' flanking sequences also facilitates production of zkun8 proteins by "gene activation" as disclosed in U.S. Patent No. 5,641,670. Briefly, expression of an endogenous zkun8 gene in a cell is altered by introducing into the zkun8 locus a DNA construct comprising at least a targeting sequence, a regulatory sequence, an exon, and an unpaired splice donor site. The targeting sequence is a zkun8 5' non-coding sequence that permits homologous recombination of the construct with the endogenous zkun8 locus, whereby the sequences within the construct become operably linked with the endogenous zkun8 coding sequence. In this way, an endogenous zkun8 promoter can be replaced or supplemented with other regulatory sequences to provide enhanced, tissue-specific, or otherwise regulated expression.

Those skilled in the art will recognize that the sequences disclosed in SEQ ID NOS:1 and 2 represent a single allele of human zkun8. Allelic variants of

these sequences can be cloned by probing cDNA or genomic libraries from different individuals according to standard procedures.

The present invention further provides counterpart polypeptides and polynucleotides from other species ("orthologs"). Of particular interest are zkun8 polypeptides from other mammalian species, including murine, porcine, ovine, bovine, canine, feline, equine, and other primate polypeptides. Orthologs of human zkun8 can be cloned using information and compositions provided by the present invention in combination with conventional cloning techniques. For example, a cDNA can be cloned using mRNA obtained from a tissue or cell type that expresses zkun8 as disclosed above. A library is then prepared from mRNA of a positive tissue or cell line. A zkun8-encoding cDNA can then be isolated by a variety of methods, such as by probing with a complete or partial human cDNA or with one or more sets of degenerate probes based on the disclosed sequence. A cDNA can also be cloned using the polymerase chain reaction, or PCR (Mullis, U.S. Patent No. 4,683,202), using primers designed from the representative human zkun8 sequence disclosed herein. Within an additional method, the cDNA library can be used to transform or transfect host cells, and expression of the cDNA of interest can be detected with an antibody to zkun8 polypeptide. Similar techniques can also be applied to the isolation of genomic clones.

Nucleic acid molecules can be used to detect the expression of a *Zkun8* gene in a biological sample. Such probe molecules include double-stranded nucleic acid molecules comprising the nucleotide sequence of SEQ ID NO:1, or a fragment thereof, as well as single-stranded nucleic acid molecules having the complement of the nucleotide sequence of SEQ ID NO:1, or a portion thereof. As used herein, the term "portion" refers to at least eight nucleotides to at least 20 or more nucleotides. Probe molecules may be DNA, RNA, oligonucleotides, and the like. Certain probes bind with regions of a *Zkun8* gene that have a low sequence similarity to comparable regions in other serine protease inhibitors.

In a basic assay, a single-stranded probe molecule is incubated with RNA, isolated from a biological sample, under conditions of temperature and ionic strength that promote base pairing between the probe and target *Zkun8* RNA species. After separating unbound probe from hybridized molecules, the amount of hybrids is detected.

Well-established hybridization methods of RNA detection include northern analysis and dot/slot blot hybridization (see, for example, Ausubel (1995) at pages 4-1 to 4-27, and Wu *et al.* (eds.), "Analysis of Gene Expression at the RNA Level," in *Methods in Gene Biotechnology*, pages 225-239 (CRC Press, Inc. 1997)). Nucleic acid probes can be detectably labeled with radioisotopes such as <sup>32</sup>P or <sup>35</sup>S.

Alternatively, *Zkun8* RNA can be detected with a nonradioactive hybridization method (see, for example, Isaac (ed.), *Protocols for Nucleic Acid Analysis by Nonradioactive Probes* (Humana Press, Inc. 1993)). Typically, nonradioactive detection is achieved by enzymatic conversion of chromogenic or chemiluminescent substrates. Illustrative nonradioactive moieties include biotin, fluorescein, and digoxigenin.

*Zkun8* oligonucleotide probes are also useful for *in vivo* diagnosis. As an illustration,  $^{18}\text{F}$ -labeled oligonucleotides can be administered to a subject and visualized by positron emission tomography (Tavittian *et al.*, *Nature Medicine* 4:467 (1998)).

Numerous diagnostic procedures take advantage of the polymerase chain reaction (PCR) to increase sensitivity of detection methods. Standard techniques for performing PCR are well-known (see, generally, Mathew (ed.), *Protocols in Human Molecular Genetics* (Humana Press, Inc. 1991), White (ed.), *PCR Protocols: Current Methods and Applications* (Humana Press, Inc. 1993), Cotter (ed.), *Molecular Diagnosis of Cancer* (Humana Press, Inc. 1996), Hanausek and Walaszek (eds.), *Tumor Marker Protocols* (Humana Press, Inc. 1998), Lo (ed.), *Clinical Applications of PCR* (Humana Press, Inc. 1998), and Meltzer (ed.), *PCR in Bioanalysis* (Humana Press, Inc. 1998)).

One variation of PCR for diagnostic assays is reverse transcriptase-PCR (RT-PCR). In the RT-PCR technique, RNA is isolated from a biological sample, reverse transcribed to cDNA, and the cDNA is incubated with *Zkun8* primers (see, for example, Wu *et al.* (eds.), "Rapid Isolation of Specific cDNAs or Genes by PCR," in *Methods in Gene Biotechnology*, pages 15-28 (CRC Press, Inc. 1997)). PCR is then performed and the products are analyzed using standard techniques.

As an illustration, RNA is isolated from biological sample using, for example, the guanidinium-thiocyanate cell lysis procedure described above. Alternatively, a solid-phase technique can be used to isolate mRNA from a cell lysate. A reverse transcription reaction can be primed with the isolated RNA using random oligonucleotides, short homopolymers of dT, or *Zkun8* anti-sense oligomers. Oligo-dT primers offer the advantage that various mRNA nucleotide sequences are amplified that can provide control target sequences. *Zkun8* sequences are amplified by the polymerase chain reaction using two flanking oligonucleotide primers that are typically 20 bases in length.

PCR amplification products can be detected using a variety of approaches. For example, PCR products can be fractionated by gel electrophoresis, and visualized by ethidium bromide staining. Alternatively, fractionated PCR products can be transferred to a membrane, hybridized with a detectably-labeled *Zkun8* probe, and examined by autoradiography. Additional alternative approaches include the use of

digoxigenin-labeled deoxyribonucleic acid triphosphates to provide chemiluminescence detection, and the C-TRAK colorimetric assay.

Another approach for detection of *Zkun8* expression is cycling probe technology, in which a single-stranded DNA target binds with an excess of DNA-RNA-DNA chimeric probe to form a complex, the RNA portion is cleaved with RNAase H, and the presence of cleaved chimeric probe is detected (see, for example, Beggs *et al.*, *J. Clin. Microbiol.* 34:2985 (1996), Bekkaoui *et al.*, *Biotechniques* 20:240 (1996)). Alternative methods for detection of *Zkun8* sequences can utilize approaches such as nucleic acid sequence-based amplification, cooperative amplification of templates by cross-hybridization, and the ligase chain reaction (see, for example, Marshall *et al.*, U.S. Patent No. 5,686,272 (1997), Dyer *et al.*, *J. Virol. Methods* 60:161 (1996), Ehricht *et al.*, *Eur. J. Biochem.* 243:358 (1997), and Chadwick *et al.*, *J. Virol. Methods* 70:59 (1998)). Other standard methods are known to those of skill in the art.

*Zkun8* probes and primers can also be used to detect and to localize *Zkun8* gene expression in tissue samples. Methods for such *in situ* hybridization are well-known to those of skill in the art (see, for example, Choo (ed.), *In Situ Hybridization Protocols* (Humana Press, Inc. 1994), Wu *et al.* (eds.), "Analysis of Cellular DNA or Abundance of mRNA by Radioactive *In Situ* Hybridization (RISH)," in *Methods in Gene Biotechnology*, pages 259-278 (CRC Press, Inc. 1997), and Wu *et al.* (eds.), "Localization of DNA or Abundance of mRNA by Fluorescence *In Situ* Hybridization (RISH)," in *Methods in Gene Biotechnology*, pages 279-289 (CRC Press, Inc. 1997)). Various additional diagnostic approaches are well-known to those of skill in the art (see, for example, Mathew (ed.), *Protocols in Human Molecular Genetics* (Humana Press, Inc. 1991), Coleman and Tsongalis, *Molecular Diagnostics* (Humana Press, Inc. 1996), and Elles, *Molecular Diagnosis of Genetic Diseases* (Humana Press, Inc., 1996)).

*Zkun8* gene has been localized to 15q26.1 of the human genome. *Zkun8* nucleotide sequences can be used in linkage-based testing for various diseases, and to determine whether a subject's chromosomes contain a mutation in the *Zkun8* gene. Detectable chromosomal aberrations at the *Zkun8* gene locus include, but are not limited to, aneuploidy, gene copy number changes, insertions, deletions, restriction site changes and rearrangements. Of particular interest are genetic alterations that inactivate a *Zkun8* gene.

Aberrations associated with a *Zkun8* locus can be detected using nucleic acid molecules of the present invention by employing molecular genetic techniques, such as restriction fragment length polymorphism analysis, short tandem repeat analysis employing PCR techniques, amplification-refractory mutation system analysis, single-

strand conformation polymorphism detection, RNase cleavage methods, denaturing gradient gel electrophoresis, fluorescence-assisted mismatch analysis, and other genetic analysis techniques known in the art (see, for example, Mathew (ed.), *Protocols in Human Molecular Genetics* (Humana Press, Inc. 1991), Marian, *Chest* 108:255 (1995),  
5 Coleman and Tsongalis, *Molecular Diagnostics* (Human Press, Inc. 1996), Elles (ed.) *Molecular Diagnosis of Genetic Diseases* (Humana Press, Inc. 1996), Landegren (ed.), *Laboratory Protocols for Mutation Detection* (Oxford University Press 1996), Birren *et al.* (eds.), *Genome Analysis, Vol. 2: Detecting Genes* (Cold Spring Harbor Laboratory Press 1998), Dracopoli *et al.* (eds.), *Current Protocols in Human Genetics* (John Wiley & Sons 1998), and Richards and Ward, "Molecular Diagnostic Testing," in *Principles of Molecular Medicine*, pages 83-88 (Humana Press, Inc. 1998)).

The protein truncation test is also useful for detecting the inactivation of a gene in which translation-terminating mutations produce only portions of the encoded protein (see, for example, Stoppa-Lyonnet *et al.*, *Blood* 91:3920 (1998)). According to  
15 this approach, RNA is isolated from a biological sample, and used to synthesize cDNA. PCR is then used to amplify the *Zkun8* target sequence and to introduce an RNA polymerase promoter, a translation initiation sequence, and an in-frame ATG triplet. PCR products are transcribed using an RNA polymerase, and the transcripts are translated *in vitro* with a T7-coupled reticulocyte lysate system. The translation  
20 products are then fractionated by SDS-PAGE to determine the lengths of the translation products. The protein truncation test is described, for example, by Dracopoli *et al.* (eds.), *Current Protocols in Human Genetics*, pages 9.11.1 - 9.11.18 (John Wiley & Sons 1998).

The present invention also contemplates kits for performing a diagnostic  
25 assay for *Zkun8* gene expression or to analyze the *Zkun8* locus of a subject. Such kits comprise nucleic acid probes, such as double-stranded nucleic acid molecules comprising the nucleotide sequence of SEQ ID NO:1, or a fragment thereof, as well as single-stranded nucleic acid molecules having the complement of the nucleotide sequence of SEQ ID NO:1, or a fragment thereof. Probe molecules may be DNA,  
30 RNA, oligonucleotides, and the like. Kits may comprise nucleic acid primers for performing PCR.

Such a kit can contain all the necessary elements to perform a nucleic acid diagnostic assay described above. A kit will comprise at least one container comprising a *Zkun8* probe or primer. The kit may also comprise a second container  
35 comprising one or more reagents capable of indicating the presence of *Zkun8* sequences. Examples of such indicator reagents include detectable labels such as radioactive labels, fluorochromes, chemiluminescent agents, and the like. A kit may



also comprise a means for conveying to the user that the *Zkun8* probes and primers are used to detect *Zkun8* gene expression. For example, written instructions may state that the enclosed nucleic acid molecules can be used to detect either a nucleic acid molecule that encodes *Zkun8*, or a nucleic acid molecule having a nucleotide sequence that is complementary to a *Zkun8*-encoding nucleotide sequence, or to analyze chromosomal sequences associated with the *Zkun8* locus. The written material can be applied directly to a container, or the written material can be provided in the form of a packaging insert.

*Zkun8* proteins, including variants of wild-type *zkun8*, are tested for activity in protease inhibition assays, a variety of which are known in the art. Preferred assays include those measuring inhibition of trypsin, chymotrypsin, plasmin, cathepsin G, and human leukocyte elastase. See, for example, Petersen et al., Eur. J. Biochem. 235:310-316, 1996. In a typical procedure, the inhibitory activity of a test compound is measured by incubating the test compound with the proteinase, then adding an appropriate substrate, typically a chromogenic peptide substrate. See, for example, Norris et al. (Biol. Chem. Hoppe-Seyler 371:37-42, 1990). Briefly, various concentrations of the inhibitor are incubated in the presence of trypsin, plasmin, and plasma kallikrein in a low-salt buffer at pH 7.4, 25°C. After 30 minutes, the residual enzymatic activity is measured by the addition of a chromogenic substrate (e.g., S2251 (D-Val-Leu-Lys-Nan) or S2302 (D-Pro-Phe-Arg-Nan), available from Kabi, Stockholm, Sweden) and a 30-minute incubation. Inhibition of enzyme activity is indicated by a decrease in absorbance at 405 nm or fluorescence  $E_m$  at 460 nm. From the results, the apparent inhibition constant  $K_i$  is calculated. The inhibition of coagulation factors (e.g., factor VIIa, factor Xa) can be measured using chromogenic substrates or in conventional coagulation assays (e.g., clotting time of normal human plasma; Dennis et al., *ibid.*).

*Zkun8* proteins can be tested in animal models of disease, particularly tumor models, models of fibrinolysis, and models of imbalance of hemostasis. Suitable models are known in the art. For example, inhibition of tumor metastasis can be assessed in mice into which cancerous cells or tumor tissue have been introduced by implantation or injection (e.g., Brown, Advan. Enzyme Regul. 35:293-301, 1995; Conway et al., Clin. Exp. Metastasis 14:115-124, 1996). Effects on fibrinolysis can be measured in a rat model wherein the enzyme batroxobin and radiolabeled fibrinogen are administered to test animals. Inhibition of fibrinogen activation by a test compound is seen as a reduction in the circulating level of the label as compared to animals not receiving the test compound. See, Lenfors and Gustafsson, Semin. Thromb. Hemost. 22:335-342, 1996. *Zkun8* proteins can be delivered to test animals by injection or

infusion, or can be produced *in vivo* by way of, for example, viral or naked DNA delivery systems or transgenic expression.

Exemplary viral delivery systems include adenovirus, herpesvirus, vaccinia virus and adeno-associated virus (AAV). Adenovirus, a double-stranded DNA virus, is currently the best studied gene transfer vector for delivery of heterologous nucleic acid (for a review, see Becker et al., Meth. Cell Biol. 43:161-189, 1994; and Douglas and Curiel, Science & Medicine 4:44-53, 1997). The adenovirus system offers several advantages: adenovirus can (i) accommodate relatively large DNA inserts; (ii) be grown to high titer; (iii) infect a broad range of mammalian cell types; and (iv) be used with a large number of available vectors containing different promoters. Also, because adenoviruses are stable in the bloodstream, they can be administered by intravenous injection. By deleting portions of the adenovirus genome, larger inserts (up to 7 kb) of heterologous DNA can be accommodated. These inserts can be incorporated into the viral DNA by direct ligation or by homologous recombination with a co-transfected plasmid. In an exemplary system, the essential E1 gene is deleted from the viral vector, and the virus will not replicate unless the E1 gene is provided by the host cell (e.g., the human 293 cell line). When intravenously administered to intact animals, adenovirus primarily targets the liver. If the adenoviral delivery system has an E1 gene deletion, the virus cannot replicate in the host cells. However, the host's tissue (e.g., liver) will express and process (and, if a signal sequence is present, secrete) the heterologous protein. Secreted proteins will enter the circulation in the highly vascularized liver, and effects on the infected animal can be determined.

An alternative method of gene delivery comprises removing cells from the body and introducing a vector into the cells as a naked DNA plasmid. The transformed cells are then re-implanted in the body. Naked DNA vectors are introduced into host cells by methods known in the art, including transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter. See, Wu et al., J. Biol. Chem. 263:14621-14624, 1988; Wu et al., J. Biol. Chem. 267:963-967, 1992; and Johnston and Tang, Meth. Cell Biol. 43:353-365, 1994.

Transgenic mice, engineered to express a zkun8 gene, and mice that exhibit a complete absence of zkun8 gene function, referred to as "knockout mice" (Snouwaert et al., Science 257:1083, 1992), can also be generated (Lowell et al., Nature 366:740-742, 1993). These mice are employed to study the zkun8 gene and the encoded protein in an *in vivo* system. Transgenic mice are particularly useful for investigating the role of zkun8 proteins in early development because they allow the

identification of developmental abnormalities or blocks resulting from the over- or underexpression of a specific factor.

The zkun8 polypeptides of the present invention, including full-length polypeptides, biologically active fragments, and fusion polypeptides can be produced in genetically engineered host cells according to conventional techniques. Suitable host cells are those cell types that can be transformed or transfected with exogenous DNA and grown in culture, and include bacteria, fungal cells, and cultured higher eukaryotic cells. Eukaryotic cells, particularly cultured cells of multicellular organisms, are preferred. Techniques for manipulating cloned DNA molecules and introducing exogenous DNA into a variety of host cells are disclosed by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989, and Ausubel et al., eds., *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc., NY, 1987.

In general, a DNA sequence encoding a zkun8 polypeptide is operably linked to other genetic elements required for its expression, generally including a transcription promoter and terminator, within an expression vector. The vector will also commonly contain one or more selectable markers and one or more origins of replication, although those skilled in the art will recognize that within certain systems selectable markers may be provided on separate vectors, and replication of the exogenous DNA may be provided by integration into the host cell genome. Selection of promoters, terminators, selectable markers, vectors and other elements is a matter of routine design within the level of ordinary skill in the art. Many such elements are described in the literature and are available through commercial suppliers.

To direct a zkun8 polypeptide into the secretory pathway of a host cell, a secretory signal sequence (also known as a leader sequence, prepro sequence or pre sequence) is provided in the expression vector. The secretory signal sequence may be that of zkun8, or may be derived from another secreted protein (e.g., t-PA) or synthesized *de novo*. The secretory signal sequence is operably linked to the zkun8 DNA sequence, i.e., the two sequences are joined in the correct reading frame and positioned to direct the newly synthesized polypeptide into the secretory pathway of the host cell. Secretory signal sequences are commonly positioned 5' to the DNA sequence encoding the polypeptide of interest, although certain signal sequences may be positioned elsewhere in the DNA sequence of interest (see, e.g., Welch et al., U.S. Patent No. 5,037,743; Holland et al., U.S. Patent No. 5,143,830).

Cultured mammalian cells are suitable hosts for use within the present invention. Methods for introducing exogenous DNA into mammalian host cells include calcium phosphate-mediated transfection (Wigler et al., *Cell* 14:725, 1978; Corsaro and

Pearson, Somatic Cell Genetics 7:603, 1981; Graham and Van der Eb, Virology 52:456, 1973), electroporation (Neumann et al., EMBO J. 1:841-845, 1982), DEAE-dextran mediated transfection (Ausubel et al., *ibid.*), and liposome-mediated transfection (Hawley-Nelson et al., Focus 15:73, 1993; Ciccarone et al., Focus 15:80, 1993). The production of recombinant polypeptides in cultured mammalian cells is disclosed, for example, by Levinson et al., U.S. Patent No. 4,713,339; Hagen et al., U.S. Patent No. 4,784,950; Palmiter et al., U.S. Patent No. 4,579,821; and Ringold, U.S. Patent No. 4,656,134. Suitable cultured mammalian cells include the COS-1 (ATCC No. CRL 1650), COS-7 (ATCC No. CRL 1651), BHK (ATCC No. CRL 1632), BHK 570 (ATCC No. CRL 10314), 293 (ATCC No. CRL 1573; Graham et al., *J. Gen. Virol.* 36:59-72, 1977) and Chinese hamster ovary (e.g. CHO-K1; ATCC No. CCL 61) cell lines. Additional suitable cell lines are known in the art and available from public depositories such as the American Type Culture Collection, 10801 University Boulevard, Manassas, VA. In general, strong transcription promoters are preferred, such as promoters from SV-40 or cytomegalovirus. See, e.g., U.S. Patent No. 4,956,288. Other suitable promoters include those from metallothionein genes (U.S. Patent Nos. 4,579,821 and 4,601,978) and the adenovirus major late promoter. Expression vectors for use in mammalian cells include pZP-1 and pZP-9, which have been deposited with the American Type Culture Collection, 10801 University Boulevard, Manassas, VA under accession numbers 98669 and 98668, respectively.

Drug selection is generally used to select for cultured mammalian cells into which foreign DNA has been inserted. Such cells are commonly referred to as "transfectants". Cells that have been cultured in the presence of the selective agent and are able to pass the gene of interest to their progeny are referred to as "stable transfectants." A preferred selectable marker is a gene encoding resistance to the antibiotic neomycin. Selection is carried out in the presence of a neomycin-type drug, such as G-418 or the like. Selection systems can also be used to increase the expression level of the gene of interest, a process referred to as "amplification." Amplification is carried out by culturing transfectants in the presence of a low level of the selective agent and then increasing the amount of selective agent to select for cells that produce high levels of the products of the introduced genes. A preferred amplifiable selectable marker is dihydrofolate reductase, which confers resistance to methotrexate. Other drug resistance genes (e.g. hygromycin resistance, multi-drug resistance, puromycin acetyltransferase) can also be used.

Other higher eukaryotic cells can also be used as hosts, including insect cells, plant cells and avian cells. The use of *Agrobacterium rhizogenes* as a vector for expressing genes in plant cells has been reviewed by Sinkar et al., J. Biosci. (Bangalore)

11:47-58, 1987. Insect cells can be infected with recombinant baculovirus vectors, which are commonly derived from *Autographa californica* multiple nuclear polyhedrosis virus (AcMNPV). DNA encoding the polypeptide of interest is inserted into the viral genome in place of the polyhedrin gene coding sequence by homologous recombination in cells infected with intact, wild-type AcMNPV and transfected with a transfer vector comprising the cloned gene operably linked to polyhedrin gene promoter, terminator, and flanking sequences. The resulting recombinant virus is used to infect host cells, typically a cell line derived from the fall armyworm, *Spodoptera frugiperda*. See, in general, Glick and Pasternak, *Molecular Biotechnology: Principles and Applications of Recombinant DNA*, ASM Press, Washington, D.C., 1994.

Fungal cells, including yeast cells, can also be used within the present invention. Yeast species of particular interest in this regard include *Saccharomyces cerevisiae*, *Pichia pastoris*, and *Pichia methanolica*. Methods for transforming *S. cerevisiae* cells with exogenous DNA and producing recombinant polypeptides therefrom are disclosed by, for example, Kawasaki, U.S. Patent No. 4,599,311; Kawasaki et al., U.S. Patent No. 4,931,373; Brake, U.S. Patent No. 4,870,008; Welch et al., U.S. Patent No. 5,037,743; and Murray et al., U.S. Patent No. 4,845,075. Transformed cells are selected by phenotype determined by the selectable marker, commonly drug resistance or the ability to grow in the absence of a particular nutrient (e.g., leucine). A preferred vector system for use in *Saccharomyces cerevisiae* is the *POT1* vector system disclosed by Kawasaki et al. (U.S. Patent No. 4,931,373), which allows transformed cells to be selected by growth in glucose-containing media. Suitable promoters and terminators for use in yeast include those from glycolytic enzyme genes (see, e.g., Kawasaki, U.S. Patent No. 4,599,311; Kingsman et al., U.S. Patent No. 4,615,974; and Bitter, U.S. Patent No. 4,977,092) and alcohol dehydrogenase genes. See also U.S. Patents Nos. 4,990,446; 5,063,154; 5,139,936 and 4,661,454. Transformation systems for other yeasts, including *Hansenula polymorpha*, *Schizosaccharomyces pombe*, *Kluyveromyces lactis*, *Kluyveromyces fragilis*, *Ustilago maydis*, *Pichia pastoris*, *Pichia methanolica*, *Pichia guilliermondii* and *Candida maltosa* are known in the art. See, for example, Gleeson et al., *J. Gen. Microbiol.* 132:3459-3465, 1986 and Cregg, U.S. Patent No. 4,882,279. *Aspergillus* cells may be utilized according to the methods of McKnight et al., U.S. Patent No. 4,935,349. Methods for transforming *Acremonium chrysogenum* are disclosed by Sumino et al., U.S. Patent No. 5,162,228. Methods for transforming *Neurospora* are disclosed by Lambowitz, U.S. Patent No. 4,486,533. Production of recombinant proteins in *Pichia methanolica* is disclosed in U.S. Patents No. 5,716,808, 5,736,383, 5,854,039, and 5,888,768.

Prokaryotic host cells, including strains of the bacteria *Escherichia coli*, *Bacillus* and other genera are also useful host cells within the present invention. Techniques for transforming these hosts and expressing foreign DNA sequences cloned therein are well known in the art (see, e.g., Sambrook et al., *ibid.*). When expressing a  
5 zkun8 polypeptide in bacteria such as *E. coli*, the polypeptide may be retained in the cytoplasm, typically as insoluble granules, or may be directed to the periplasmic space by a bacterial secretion sequence. In the former case, the cells are lysed, and the granules are recovered and denatured using, for example, guanidine isothiocyanate or urea. The denatured polypeptide can then be refolded and dimerized by diluting the  
10 denaturant, such as by dialysis against a solution of urea and a combination of reduced and oxidized glutathione, followed by dialysis against a buffered saline solution. In the latter case, the polypeptide can be recovered from the periplasmic space in a soluble and functional form by disrupting the cells (by, for example, sonication or osmotic shock) to release the contents of the periplasmic space and recovering the protein,  
15 thereby obviating the need for denaturation and refolding.

Transformed or transfected host cells are cultured according to conventional procedures in a culture medium containing nutrients and other components required for the growth of the chosen host cells. A variety of suitable media, including defined media and complex media, are known in the art and generally  
20 include a carbon source, a nitrogen source, essential amino acids, vitamins and minerals. Media may also contain such components as growth factors or serum, as required. The growth medium will generally select for cells containing the exogenously added DNA by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker carried on the expression vector or co-transfected into the host cell. *P. methanolica* cells are cultured in a medium comprising  
25 adequate sources of carbon, nitrogen and trace nutrients at a temperature of about 25°C to 35°C. Liquid cultures are provided with sufficient aeration by conventional means, such as shaking of small flasks or sparging of fermentors.

It is preferred to purify the proteins of the present invention to  $\geq 80\%$   
30 purity, more preferably to  $\geq 90\%$  purity, even more preferably  $\geq 95\%$  purity, and particularly preferred is a pharmaceutically pure state, that is greater than 99.9% pure with respect to contaminating macromolecules, particularly other proteins and nucleic acids, and free of infectious and pyrogenic agents. Preferably, a purified protein is substantially free of other proteins, particularly other proteins of animal origin.

35 Zkun8 proteins are purified by conventional protein purification methods, typically by a combination of chromatographic techniques. Polypeptides comprising a polyhistidine affinity tag (typically about 6 histidine residues) are purified

by affinity chromatography on a nickel chelate resin. See, for example, Houchuli et al., Bio/Technol. 6: 1321-1325, 1988.

The polypeptides of the present invention can also be isolated by exploitation of their heparin binding properties. For a review, see, Burgess et al., Ann. Rev. of Biochem. 58:575-606, 1989. Members of the FGF family can be purified to apparent homogeneity by heparin-Sepharose affinity chromatography (Gospodarowicz et al., Proc. Natl. Acad. Sci. 81:6963-6967, 1984) and eluted using linear step gradients of NaCl (Ron et al., J. Biol. Chem. 268(4):2984-2988, 1993; Chromatography: Principles & Methods, pp. 77-80, Pharmacia LKB Biotechnology, Uppsala, Sweden, 1993; in "Immobilized Affinity Ligand Techniques", Hermanson et al., eds., pp. 165-167, Academic Press, San Diego, 1992; Kjellen et al., Ann. Rev. Biochem. Ann. Rev. Biochem. 60:443-474, 1991; and Ke et al., Protein Expr. Purif. 3(6):497-507, 1992.)

Using methods known in the art, zkun8 proteins can be produced glycosylated or non-glycosylated; pegylated or non-pegylated; and may or may not include an initial methionine amino acid residue.

The zkun8 proteins are contemplated for use in the treatment or prevention of conditions associated with excessive proteinase activity, in particular an excess of trypsin, plasmin, kallikrein, elastase, cathepsin G, proteinase-3, thrombin, factor VIIa, factor IXa, factor Xa, factor XIa, factor XIIa, or matrix metalloproteinases. Such conditions include, but are not limited to, acute pancreatitis, cardiopulmonary bypass (CPB)-induced pulmonary injury, allergy-induced protease release, deep vein thrombosis, myocardial infarction, shock (including septic shock), hyperfibrinolytic hemorrhage, emphysema, rheumatoid arthritis, adult respiratory distress syndrome, chronic inflammatory bowel disease, psoriasis, and other inflammatory conditions. Zkun8 proteins are also contemplated for use in preservation of platelet function, organ preservation, and wound healing.

Zkun8 proteins may be useful in the treatment of conditions arising from an imbalance in hemostasis, including acquired coagulopathies, primary fibrinolysis and fibrinolysis due to cirrhosis, and complications from high-dose thrombolytic therapy. Acquired coagulopathies can result from liver disease, uremia, acute disseminated intravascular coagulation, post-cardiopulmonary bypass, stroke, massive transfusion, or Warfarin overdose (Humphries, Transfusion Medicine 1:1181-1201, 1994). A deficiency or dysfunction in any of the procoagulant mechanisms predisposes the patient to either spontaneous hemorrhage or excess blood loss associated with trauma or surgery. Acquired coagulopathies usually involve a combination of deficiencies, such as deficiencies of a plurality of coagulation factors, and/or platelet dysfunction. In addition, patients with liver disease commonly experience increased

fibrinolysis due to an inability to maintain normal levels of  $\alpha_2$ -antiplasmin and/or decreased hepatic clearance of plasminogen activators (Shuman, *Hemorrhagic Disorders*, in Bennet and Plum, eds. Cecil Textbook of Medicine, 20th ed., W.B. Saunders Co., 1996). Primary fibrinolysis results from a massive release of plasminogen activator. Conditions associated with primary fibrinolysis include carcinoma of the prostate, acute promyelocytic leukemia, hemangiomas, and sustained release of plasminogen activator by endothelial cells due to injection of venoms. The condition becomes critical when enough plasmin is activated to deplete the circulating level of  $\alpha_2$ -antiplasmin (Shuman, *ibid.*). Data suggest that plasmin on endothelial cells may be related to the pathophysiology of bleeding or rethrombosis observed in patients undergoing high-dose thrombolytic therapy for thrombosis. Plasmin may cause further damage to the thrombogenic surface of blood vessels after thrombolysis, which may result in rethrombosis (Okajima, J. Lab. Clin. Med. 126:1377-1384, 1995).

Additional antithrombotic uses of zkun8 proteins include treatment or prevention of deep vein thrombosis, pulmonary embolism, and post-surgical thrombosis.

Zkun8 proteins may also be used within methods for inhibiting blood coagulation in mammals, such as in the treatment of disseminated intravascular coagulation. Zkun8 proteins may thus be used in place of known anticoagulants such as heparin, coumarin, and anti-thrombin III. Such methods will generally include administration of the protein in an amount sufficient to produce a clinically significant inhibition of blood coagulation. Such amounts will vary with the nature of the condition to be treated, but can be predicted on the basis of known assays and experimental animal models, and will in general be within the ranges disclosed below.

Zkun8 proteins may also find therapeutic use in the blockage of proteolytic tissue degradation. Proteolysis of extracellular matrix, connective tissue, and other tissues and organs is an element of many diseases. This tissue destruction is believed to be initiated when plasmin activates one or more matrix metalloproteinases (e.g., collagenase and metallo-elastases). Inhibition of plasmin by zkun8 proteins may thus be beneficial in the treatment of these conditions.

Matrix metalloproteinases (MMPs) are believed to play a role in metastases of cancers, abdominal aortic aneurysm, multiple sclerosis, rheumatoid arthritis, osteoarthritis, trauma and hemorrhagic shock, and corneal ulcers. MMPs produced by tumor cells break down and remodel tissue matrices during the process of metastatic spread. There is evidence to suggest that MMP inhibitors may block this activity (Brown, Advan. Enzyme Regul. 35:293-301, 1995). Abdominal aortic aneurysm is characterized by the degradation of extracellular matrix and loss of



structural integrity of the aortic wall. Data suggest that plasmin may be important in the sequence of events leading to this destruction of aortic matrix (Jean-Claude et al., Surgery 116:472-478, 1994). Proteolytic enzymes are also believed to contribute to the inflammatory tissue damage of multiple sclerosis (Gijbels, J. Clin. Invest. 94:2177-2182, 1994). Rheumatoid arthritis is a chronic, systemic inflammatory disease predominantly affecting joints and other connective tissues, wherein proliferating inflammatory tissue (panus) may cause joint deformities and dysfunction (see, Arnett, in Cecil Textbook of Medicine, *ibid.*). Osteoarthritis is a chronic disease causing deterioration of the joint cartilage and other joint tissues and the formation of new bone (bone spurs) at the margins of the joints. There is evidence that MMPs participate in the degradation of collagen in the matrix of osteoarthritic articular cartilage. Inhibition of MMPs results in the inhibition of the removal of collagen from cartilage matrix (Spirito, Inflam. Res. 44 (supp. 2):S131-S132, 1995; O'Byrne, Inflam. Res. 44 (supp. 2):S117-S118, 1995; Karran, Ann. Rheumatic Disease 54:662-669, 1995). Zkun8 proteins may also be useful in the treatment of trauma and hemorrhagic shock. Data suggest that administration of an MMP inhibitor after hemorrhage improves cardiovascular response, hepatocellular function, and microvascular blood flow in various organs (Wang, Shock 6:377-382, 1996). Corneal ulcers, which can result in blindness, manifest as a breakdown of the collagenous stromal tissue. Damage due to thermal or chemical injury to corneal surfaces often results in a chronic wound-healing situation. There is direct evidence for the role of MMPs in basement membrane defects associated with failure to re-epithelialize in cornea or skin (Fini, Am. J. Pathol. 149:1287-1302, 1996).

The zkun8 proteins of the present invention may be combined with other therapeutic agents to augment the activity (e.g., antithrombotic or anticoagulant activity) of such agents. For example, a zkun8 protein may be used in combination with tissue plasminogen activator in thrombolytic therapy.

The ovarian cycle in mammals includes the growth and maturation of follicles, followed by ovulation and transformation of follicles into corpea lutea. The physiological events in the ovarian cycle are dependent on interactions between hormones and cells within the hypothalamic-pituitary-ovarian axis, including gonadotropin releasing hormone (GnRH), LH, and FSH. In addition, estradiol, synthesized in the follicle, primes the hypothalamic-pituitary axis and is required for the mid-cycle surge of gonadotropin that stimulates the resumption of oocyte meiosis and leads to ovulation and subsequent extrusion of an oocyte from the follicle. This gonadotropin surge also promotes the differentiation of the follicular cells from secreting estradiol to secreting progesterone. Progesterone, secreted by the corpus

luteum, is needed for uterine development required for the implantation of fertilized oocytes. The central role of hypothalamic-pituitary-gonadal hormones in the ovarian cycle and reproductive cascade, and the role of sex steroids on target tissues and organs, e.g., uterus, breast, adipose, bones and liver, has made modulators of their activity desirable for therapeutic applications. Such applications include treatments for precocious puberty, endometriosis, uterine leiomyomata, hirsutism, infertility, premenstrual syndrome (PMS), amenorrhea, and as contraceptive agents.

Zkun8 is expressed in ovarian tissue, and therefore, will be associated with ovarian function, i.e. reproduction and hormonal homeostasis. Zkun8 polypeptides, agonists and antagonists which modulate the actions of reproductive hormones can be of therapeutic value. Such molecules can also be useful for modulating steroidogenesis, both *in vivo* and *in vitro*, and modulating aspects of the ovarian cycle such as oocyte maturation, ovarian cell-cell interactions, follicular development and rupture, luteal function, and promoting uterine implantation of fertilized oocytes. Molecules which modulate hormone action can be beneficial therapeutics for use prior to or at onset of puberty. For example, puberty in females is marked by an establishment of feed-back loops to control hormone levels and hormone production. Abnormalities resulting from hormone imbalances during puberty have been observed and include precocious puberty, where pubertal changes occur in females prior to the age of 8. Hormone-modulating molecules, can be used, in this case, to suppress hormone secretion and delay onset of puberty.

The level and ratio of gonadotropin and steroid hormones can be used to assess the existence of hormonal imbalances associated with diseases, as well as determine whether normal hormonal balance has been restored after administration of a therapeutic agent. Determination of estradiol, progesterone, LH, and FSH, for example, from serum is known by one of skill in the art. Such assays can be used to monitor the hormone levels after administration of zkun8 *in vivo*, or in a transgenic mouse model where the zkun8 gene is expressed or the murine ortholog is deleted. Thus, as a hormone-modulating molecule, zkun8 polypeptide can have therapeutic application for treating, for example, breakthrough menopausal bleeding, as part of a therapeutic regime for pregnancy support, or for treating symptoms associated with polycystic ovarian syndrome (PCOS), PMS and menopause. In addition, other *in vivo* rodent models are known in the art to assay effects of zkun8 polypeptide on, for example, polycystic ovarian syndrome (PCOS).

Proteins of the present invention may also be used in applications for enhancing fertilization during assisted reproduction in humans and in animals. Such assisted reproduction methods are known in the art and include artificial insemination,

*in vitro* fertilization, embryo transfer, and gamete intrafallopian transfer. Such methods are useful for assisting those who may have physiological or metabolic disorders that prevent or impede natural conception. Such methods are also used in animal breeding programs, e.g., for livestock, racehorses, domestic and wild animals, and could be used as methods for the creation of transgenic animals. Zkun8 polypeptides could be used in the induction of ovulation, either independently or in conjunction with a regimen of gonadotropins or agents such as clomiphene citrate or bromocriptine (Speroff et al., Induction of ovulation, Clinical Gynecologic Endocrinology and Infertility, 5<sup>th</sup> ed., Baltimore, Williams & Wilkins, 1994). As such, proteins of the present invention can be administered to the recipient prior to fertilization or combined with the sperm, an egg or an egg-sperm mixture prior to *in vitro* or *in vivo* fertilization. Such proteins can also be mixed with oocytes prior to cryopreservation to enhance viability of the preserved oocytes for use in assisted reproduction.

The zkun8 polypeptides, agonists and antagonists of the present invention may be directly used as or incorporated into therapies for treating reproductive disorders. Disorders such as luteal phase deficiency would benefit from such therapy (Soules, "Luteal phase deficiency: A subtle abnormality of ovulation" in, Infertility: Evaluation and Treatment, Keye et al., eds., Philadelphia, WB Saunders, 1995). Moreover, administration of gonadotropin-releasing hormone is shown to stimulate reproductive behavior (Riskin and Moss, Res. Bull. 11:481-5, 1983; Kadar et al., Physiol. Behav. 51:601-5, 1992 and Silver et al., J. Neuroendocrin. 4:207-10, 199; King and Millar, Cell. Mol. Neurobiol., 15:5-23, 1995). Given the high prevalence of sexual dysfunction and impotence in humans, molecules, such as zkun8, which may modulate or enhance gonadotropin activity can find application in developing treatments for these conditions.

Doses of zkun8 proteins will vary according to the severity of the condition being treated and may range from approximately 10 µg/kg to 10 mg/kg body weight, preferably 100 µg/kg to 5 mg/kg, more preferably 100 µg/kg to 1 mg/kg. The proteins formulated in a pharmaceutically acceptable carrier or vehicle. It is preferred to prepare them in a form suitable for injection or infusion, such as by dilution with sterile water, an isotonic saline or glucose solution, or similar vehicle. In the alternative, the protein may be packaged as a lyophilized powder, optionally in combination with a pre-measured diluent, and resuspended immediately prior to use. Pharmaceutical compositions may further include one or more excipients, preservatives, solubilizers, buffering agents, albumin to prevent protein loss on vial surfaces, etc. Formulation methods are within the level of ordinary skill in the art. See, Remington:

The Science and Practice of Pharmacy, Gennaro, ed., Mack Publishing Co., Easton, PA, 19th ed., 1995.

Gene therapy provides an alternative therapeutic approach for delivery of zkun8 proteins. If a mammal has a mutated or absent zkun8 gene, a polynucleotide encoding a zkun8 protein can be introduced into the cells of the mammal. In one embodiment, a gene encoding a zkun8 protein is introduced *in vivo* in a viral vector. Such vectors include an attenuated or defective DNA virus, such as herpes simplex virus (HSV), papillomavirus, Epstein Barr virus (EBV), adenovirus, adeno-associated virus (AAV), and the like. Defective viruses, which entirely or almost entirely lack viral genes, are preferred. A defective virus is not infective after introduction into a cell. Use of defective viral vectors allows for administration to cells in a specific, localized area, without concern that the vector can infect other cells. Examples of particular vectors include, without limitation, a defective herpes simplex virus 1 (HSV1) vector (Kaplitt et al., Molec. Cell. Neurosci. 2:320-30, 1991); an attenuated adenovirus vector, such as the vector described by Stratford-Perricaudet et al., J. Clin. Invest. 90:626-30, 1992; and a defective adeno-associated virus vector (Samulski et al., J. Virol. 61:3096-101, 1987; Samulski et al., J. Virol. 63:3822-8, 1989).

Within another embodiment, a zkun8 polynucleotide can be introduced in a retroviral vector, as described, for example, by Anderson et al., U.S. Patent No. 5,399,346; Mann et al., Cell 33:153, 1983; Temin et al., U.S. Patent No. 4,650,764; Temin et al., U.S. Patent No. 4,980,289; Markowitz et al., J. Virol. 62:1120, 1988; Temin et al., U.S. Patent No. 5,124,263; Dougherty et al., WIPO Publication No. WO 95/07358; and Kuo et al., Blood 82:845, 1993. Alternatively, the vector can be introduced by lipofection *in vivo* using liposomes. Synthetic cationic lipids can be used to prepare liposomes for *in vivo* transfection of a gene encoding a marker (Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7, 1987; Mackey et al., Proc. Natl. Acad. Sci. USA 85:8027-31, 1988).

Within a further embodiment, target cells are removed from the body, and a vector is introduced into the cells as a naked DNA plasmid. The transformed cells are then re-implanted into the body. Naked DNA vectors for gene therapy can be introduced into the desired host cells by methods known in the art, e.g., transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun or use of a DNA vector transporter. See, for example, Wu et al., J. Biol. Chem. 267:963-7, 1992; Wu et al., J. Biol. Chem. 263:14621-4, 1988.

Zkun8 proteins can also be used to prepare antibodies that specifically bind to zkun8 proteins. As used herein, the term "antibodies" includes polyclonal

antibodies, monoclonal antibodies, antigen-binding fragments thereof such as F(ab')<sub>2</sub> and Fab fragments, single chain antibodies, and the like, including genetically engineered antibodies. Non-human antibodies can be humanized by grafting only non-human CDRs onto human framework and constant regions, or by incorporating the entire non-human variable domains (optionally "cloaking" them with a human-like surface by replacement of exposed residues, wherein the result is a "veneered" antibody). In some instances, humanized antibodies may retain non-human residues within the human variable region framework domains to enhance proper binding characteristics. Through humanizing antibodies, biological half-life may be increased, and the potential for adverse immune reactions upon administration to humans is reduced. One skilled in the art can generate humanized antibodies with specific and different constant domains (i.e., different Ig subclasses) to facilitate or inhibit various immune functions associated with particular antibody constant domains. Alternative techniques for generating or selecting antibodies useful herein include *in vitro* exposure of lymphocytes to a zkun8 protein, and selection of antibody display libraries in phage or similar vectors (for instance, through use of immobilized or labeled zkun8 polypeptide). Antibodies are defined to be specifically binding if they bind to a zkun8 protein with an affinity at least 10-fold greater than the binding affinity to control (non-zkun8) polypeptide. It is preferred that the antibodies exhibit a binding affinity ( $K_d$ ) of  $10^6 M^{-1}$  or greater, preferably  $10^7 M^{-1}$  or greater, more preferably  $10^8 M^{-1}$  or greater, and most preferably  $10^9 M^{-1}$  or greater. The affinity of a monoclonal antibody can be readily determined by one of ordinary skill in the art (see, for example, Scatchard, Ann. NY Acad. Sci. 51: 660-672, 1949).

Methods for preparing polyclonal and monoclonal antibodies are well known in the art (see for example, Hurrell, J. G. R., Ed., *Monoclonal Hybridoma Antibodies: Techniques and Applications*, CRC Press, Inc., Boca Raton, FL, 1982). As would be evident to one of ordinary skill in the art, polyclonal antibodies can be generated from a variety of warm-blooded animals such as horses, cows, goats, sheep, dogs, chickens, rabbits, mice, and rats. The immunogenicity of a zkun8 protein may be increased through the use of an adjuvant such as alum (aluminum hydroxide) or Freund's complete or incomplete adjuvant. Polypeptides useful for immunization also include fusion polypeptides, such as fusions of a zkun8 protein or a portion thereof with an immunoglobulin polypeptide or with maltose binding protein. The polypeptide immunogen may be a full-length molecule or a portion thereof. If the polypeptide portion is "haptene-like", such portion may be advantageously joined or linked to a macromolecular carrier (such as keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA) or tetanus toxoid) for immunization.

Immunogenic zkun8 polypeptides may be as small as 5 residues. It is preferred to use polypeptides that are hydrophilic or comprise a hydrophilic region. A preferred such region of SEQ ID NO:2 includes residues 135-140, 335-340, 248-253, 490-495, and 63-68.

5 A variety of assays known to those skilled in the art can be utilized to detect antibodies that specifically bind to a zkun8 protein. Exemplary assays are described in detail in *Antibodies: A Laboratory Manual*, Harlow and Lane (Eds.), Cold Spring Harbor Laboratory Press, 1988. Representative examples of such assays include concurrent immunoelectrophoresis, radio-immunoassays, radio-immunoprecipitations, 10 enzyme-linked immunosorbent assays (ELISA), dot blot assays, Western blot assays, inhibition or competition assays, and sandwich assays.

Antibodies to zkun8 may be used for affinity purification of zkun8 proteins; within diagnostic assays for determining circulating levels of zkun8 proteins; for detecting or quantitating soluble zkun8 protein as a marker of underlying pathology 15 or disease; for immunolocalization within whole animals or tissue sections, including immunodiagnostic applications; for immunohistochemistry; for screening expression libraries; and for other uses that will be evident to those skilled in the art. For certain applications, including *in vitro* and *in vivo* diagnostic uses, it is advantageous to employ labeled antibodies. Suitable direct tags or labels include radionuclides, enzymes, 20 substrates, cofactors, inhibitors, fluorescent markers, chemiluminescent markers, magnetic particles and the like; indirect tags or labels may feature use of biotin-avidin or other complement/anti-complement pairs as intermediates.

Zkun8 proteins may be used in the laboratory or commercial preparation of proteins from cultured cells. The proteins can be used alone to inhibit specific 25 proteolysis or can be combined with other proteinase inhibitors to provide a "cocktail" with a broad spectrum of activity. Of particular interest is the inhibition of cellular proteases, which can be release during cell lysis. The proteins can also be used in the laboratory as a tissue culture additive to prevent cell detachment.

Zkun8 polypeptides can also be used to teach analytical skills such as 30 mass spectrometry, circular dichroism, to determine conformation, especially of the four alpha helices, x-ray crystallography to determine the three-dimensional structure in atomic detail, nuclear magnetic resonance spectroscopy to reveal the structure of proteins in solution. For example, a kit containing the Zkun8 can be given to the student to analyze. Since the amino acid sequence would be known by the instructor, the 35 protein can be given to the student as a test to determine the skills or develop the skills of the student, the instructor would then know whether or not the student has correctly

analyzed the polypeptide. Since every polypeptide is unique, the educational utility of Zkun8 would be unique unto itself.

5 The antibodies which bind specifically to Zkun8 can be used as a teaching aid to instruct students how to prepare affinity chromatography columns to purify Zkun8, cloning and sequencing the polynucleotide that encodes an antibody and thus as a practicum for teaching a student how to design humanized antibodies. The *Zkun8* gene, polypeptide, or antibody would then be packaged by reagent companies and sold to educational institutions so that the students gain skill in art of molecular biology. Because each gene and protein is unique, each gene and protein creates unique  
10 challenges and learning experiences for students in a lab practicum. Such educational kits containing the *Zkun8* gene, polypeptide, or antibody are considered within the scope of the present invention.

Thus in summary, the present invention includes, but is not limited to,  
15 certain embodiments described throughout the specification. For example, one aspect of the present invention is an isolated polypeptide comprising a sequence of amino acid residues that is at least 90% identical to the sequence shown in SEQ ID NO: 2 from residues 328-378 and/or residues 386-436 of SEQ ID NO: 2. In another embodiment, the isolated polypeptide comprises sequences that are identical to the sequence shown  
20 in SEQ ID NO: 2 from residues 328-378 and/or residues 386-436 of SEQ ID NO: 2. In another embodiment, the present invention includes a polypeptide that comprises a sequence of amino acid residues as shown in SEQ ID NO: 2 from residues 324-381 or residues 382-440.

An another embodiment, the first kunitz domain polypeptide is shown as  
25 a motif, with certain substitutions that are expected to maintain some protease inhibitor activity. In one embodiment this sequence is represented in SEQ ID NO: 4. In another embodiment, the second kunitz domain polypeptide is shown in SEQ ID NO: 5 as a motif, with certain substitutions that are expected to maintain some protease inhibitor activity. Thus, the present invention includes polypeptides and proteins that comprise  
30 the sequence of amino acid residues as shown in SEQ ID NO: 4 and/or SEQ ID NO: 5. For example, a polypeptide can comprise a first kunitz domain as shown in either SEQ ID NO: 2 from residues 328-378 or as shown in SEQ ID NO: 4 from residues 1-51. A polypeptide comprising a second kunitz domain as shown in either SEQ ID NO: 2 from residues 386-436 or SEQ ID NO: 5 from residues 1-51 are included, as are  
35 polypeptides, proteins, and fusion proteins comprising both the first and second kunitz domains.

Another aspect of the present includes polypeptides and fusion proteins comprising an isolated polypeptide comprising a sequence of amino acid residues selected from the group consisting of: (a) amino acid residues 1-34 of SEQ ID NO: 2; (b) amino acid residues 35-98 of SEQ ID NO: 2; (c) amino residues 101-180 of SEQ ID NO: 2; (d) amino acid residues 227-310 of SEQ ID NO: 2; (e) amino acid residues 324-384 of SEQ ID NO: 2; (f) amino acid residues 382-440 of SEQ ID NO: 2; and (g) amino acid residues 441-576 of SEQ ID NO: 2.

In other aspects the present invention includes polynucleotide molecules that encode the polypeptides and proteins described herein, as well as expression vectors containing the polynucleotide molecules, transcription promoters and transcription terminators, cells expressing the polynucleotide molecules and methods of producing the polypeptides and proteins using the cultured cells described herein. Nucleotide sequence corresponding to the amino acid sequence of SEQ ID NO: 2 is shown in SEQ ID NO: 1, and the degenerate nucleotide sequence is shown in SEQ ID NO: 3. One of ordinary skill in the art would recognize that when describing an amino acid sequence, the nucleotide sequence encoding for those amino acids can be identified from SEQ ID NOS: 1 and 3.

Certain other aspects of the present invention will include antibodies that specifically bind the polypeptides and proteins described herein. Also included are methods for using the molecules of the present invention. For example, the present invention includes a method of inhibiting protease degradation or activity in a composition containing plasma proteins comprising adding a zkun8 polypeptide composition comprising a sequence of amino acid residues as shown in SEQ ID NO: 2 from amino acid residue 324 to amino acid residue 381 or as shown in SEQ ID NO: 2 from amino acid residue 382 to amino acid residue 440 to the composition containing plasma proteins in an amount sufficient to reduce degradation of the composition by proteases or protease activity in the composition. In another embodiment of the method, the reduction of degradation or activity is determined by chromogenic substrate assays or clotting time assays.

The invention is further illustrated by the following non-limiting example.



## EXAMPLES

Example 15 Isolation of zkun8 cDNA

To obtain a Zkun8 cDNA clone, cDNA is prepared from ovary using a commercially available kit (Marathon™ cDNA Amplification Kit from Clontech Laboratories, Inc., Palo Alto, CA) and an oligo(dT) primer. To amplify the zkun8 DNA, 5 µl each of 1/100 diluted cDNAs, 20 pmoles each of two oligonucleotide primers designed from SEQ ID NO:1, and 1 U of a 2:1 mixture of ExTaq™ DNA polymerase (TaKaRa Biomedicals) and Pfu DNA polymerase (Stratagene, La Jolla, CA) (*ExTaq/Pfu*) are used in a 25-µl reaction mixture. The reaction mixture is incubated at 94°C for 2 minutes; 25 cycles of 94°C for 15 seconds, 66°C for 20 seconds, and 72°C for 30 seconds; and a 1-minute incubation at 72°C. 1 µl each of 1/100 diluted first PCR product is used as template for a nested PCR. 20 pmoles each of two additional oligonucleotide primers and 1 U of *ExTaq/Pfu* are used in 25 µl reaction mixtures. The mixtures are incubated at 94°C for 2 minutes; 2 cycles of 94°C for 15 seconds, 66°C for 20 seconds, 72°C for 30 seconds; 25 cycles of 94°C for 15 seconds, 64°C for 20 seconds, 72°C for 30 seconds; and a 1-minute incubation at 72°C. The PCR products are gel purified and sequenced to confirm their identity.

To construct expression vectors for the zkun8 Kunitz domains, PCR is performed on cDNA prepared from ovary as disclosed above. Primers are designed such that the PCR product will encode an intact Kunitz domain with restriction sites Bam HI in the sense primer and Xho I in the antisense primer to facilitate subcloning into an expression vector. 5 µl of 1/100 diluted cDNA, 20 pmoles of each oligonucleotide primer, and 1 U of *ExTaq/Pfu* are used in 25 µl reaction mixtures. The mixtures are incubated at 94°C for 2 minutes; 3 cycles of 94°C for 30 seconds, 50°C for 30 seconds, 72°C for 30 seconds; 35 cycles of 94°C for 30 seconds, 68°C for 30 seconds; and a 7-minute incubation at 72°C. The PCR product is gel purified and restriction digested with Bam HI and Xho I overnight.

A mammalian expression vector was constructed with the dihydrofolate reductase gene selectable marker under control of the SV40 early promoter, SV40 polyadenylation site, a cloning site to insert the gene of interest under control of the mouse metallothionein 1 (MT-1) promoter and the hGH polyadenylation site. The expression vector was designated pZP-9 and has been deposited at the American Type Culture Collection, 10801 University Boulevard, Manassas, VA under accession no 98668. To facilitate protein purification, the pZP9 vector was modified by addition of a

tissue plasminogen activator (t-PA) secretory signal sequence (see U.S. Patent No. 5,641,655) and a GluGlu tag sequence (SEQ ID NO:6) between the MT-1 promoter and hGH terminator. The t-PA secretory signal sequence replaces the native secretory signal sequence for DNAs encoding polypeptides of interest that are inserted into this vector, and expression results in an N-terminally tagged protein. The N-terminally tagged vector was designated pZP9NEE. The vector pZP9NEE is digested with Bam HI and Xho I, and the zkun8 fragment is inserted. The resulting construct is confirmed by sequencing.

## 10 Example 2

### Activity Assays

#### A. Trypsin Inhibitory Activity Assay on Mammalian Cell Culture Supernatants

Conditioned media from cells expressing Kunitz-type inhibitors is assayed for trypsin inhibitor activity. For each clone, 20-100  $\mu$ l of conditioned medium is added to a solution containing 2.4  $\mu$ g/ml trypsin (Worthington Biochemical, Freehold, NJ) in 100 mM NaCl, 50 mM Tris (pH 7.4) to give a final volume of 300  $\mu$ l. The reactions are incubated at 23°C for 30 minutes after which 20  $\mu$ l of 10 mM chromogenic substrate S-2251 (D-Val-Leu-Lys-Nan; Chromogenix, AB, Mölndal, Sweden) is added to a final concentration of 0.6 mM. The residual trypsin activity is measured by absorbance at 405 nm.

#### B. Activity Assay on Yeast Culture Supernatants

Trypsin inhibitory activity is measured on the spent media from cultures of yeast transformants described in Example 3 by diluting 3.2  $\mu$ l of each spent medium sample with 80  $\mu$ l of assay buffer (50 mM Tris HCl, pH 7.4, 100 mM NaCl, 2 mM  $\text{CaCl}_2$ , 0.1% w/v PEG 20,000). The diluted supernatant is added to 80 ml of 133 nM bovine trypsin (Novo Nordisk A/S, Copenhagen, DK) diluted in assay buffer, and the mixture is incubated for 10 minutes at room temperature. After incubation, 100 ml of 1.8 mM peptidyl nitroanilide substrate S2251 (D-Val-Leu-Lys-Nan; Kabi) diluted in assay buffer is added to each sample, and the samples are incubated with the substrate for 30 minutes. Trypsin inhibitory activity is indicated by a colorless solution. A control reaction, which results in a yellow solution, is produced by a supernatant from a yeast strain not expressing any Kunitz-type inhibitor.

Example 3Purification of Kunitz-Type Inhibitors

## A. Purification of Kunitz-Type Inhibitors from Transfected Mammalian Cell Culture Supernatants

zkun8 is purified from conditioned medium by sequential application of heparin agarose, MONO Q, MONO S and SUPEROSE 12 chromatography as described in more detail below. Conditioned serum-free media is adjusted to pH 7.5 with 1 N NaOH and filtered through a 0.22- $\mu$ m filter. A 2.6 x 35 cm heparin sepharose column (Pharmacia Biotech Inc., Piscataway, NJ) is equilibrated at 4°C with Buffer A (50 mM Tris-HCl (pH 7.5), 10% glycerol). The filtered media is applied to the equilibrated column at a flow rate of 3 ml/min. Following sample application, the column is washed with Buffer A containing 0.2 M NaCl. zkun8 activity, as judged by its ability to inhibit trypsin is eluted from the column with Buffer A containing 1 M NaCl. The eluent from the heparin sepharose column is dialyzed at 4°C against 25 mM Tris-HCl (pH 7.5), 10% glycerol. The retentate is subjected to FPLC (Pharmacia Biotech Inc.) on a 5 x 50 mm column containing an anion exchanger with quaternary amine groups crosslinked to a beaded hydrophylic resin such as a MONO Q (MONO Q HR 5/5; Pharmacia Biotech Inc., Piscataway, NJ) or the like that has been equilibrated with 25 mM Tris-HCl (pH 7.5), 10% glycerol at room temperature. zkun8 is eluted from the column in a linear NaCl gradient (from 0-0.5 M NaCl) at a flow rate of 1 ml/min. The zkun8 fractions are pooled and dialyzed against 25 mM sodium citrate (pH 5.0), 10 % glycerol. The retentate is then subjected to FPLC at room temperature on a 5 x 50 mm column containing a cation exchanger with charged sulfonic groups coupled to a beaded hydrophylic resin such as MONO S (MONO S HR 5/5, Pharmacia Biotech Inc.) or the like at a flow rate of 0.5 ml/min. zkun8 activity is eluted from the MONO S column with a gradient elution from 25 mM sodium citrate (pH 5.0), 10% glycerol to 25 mM Tris-HCl (pH 7.5), 10% glycerol, 1 M NaCl. Fractions containing zkun8 activity are pooled and concentrated to approximately 1 ml by ultrafiltration. The concentrated samples are subjected to FPLC across a cross-linked agarose gel filtration matrix having a porosity suitable for the separation of proteins from  $1 \times 10^3$  to  $3 \times 10^5$  MW such as SUPEROSE 12 (Pharmacia Biotech Inc., Piscataway, NJ) or the like at room temperature in 50 mM Tris-HCl (pH 7.5), 100 mM NaCl. Fractions eluted from the FPLC with zkun8 activity are subjected to SDS-PAGE, and pure fractions are pooled and stored at -80°C.

## B. Purification of Kunitz-Type Inhibitors from Yeast Culture Supernatants

Kunitz-type inhibitors are purified from yeast culture supernatants essentially as described by Norris et al. (ibid.; which is incorporated herein by reference). Selected transformants are grown in 10 liters of YEPD for approximately 40 hours at 30°C until an OD<sub>600</sub> of approximately 25 has been reached. The culture is centrifuged, and the supernatant is decanted.

For purification, a 300 ml-1000 ml aliquot of supernatant is adjusted to pH 2.3 and applied to a column holding 8 ml of S-Sepharose (Pharmacia-LKB Biotechnology AS, Alleroed, Denmark) that has been previously equilibrated with 20 mM Bicine, pH 8.7 (Sigma Chemical Co., St. Louis, MO). After the column has been extensively washed with 20 mM Bicine, pH 8.7, the Kunitz-type inhibitor is eluted with 30 ml of 20 mM Bicine, pH 8.7 containing 1 M NaCl. The eluted material is desalted by application to a Sephadex G-25 column (Pharmacia-LKB Biotechnology AS, Alleroed, Denmark; 2.5 x 30 cm) that has been equilibrated with 20 mM NH<sub>4</sub>HCO<sub>3</sub>, pH 7.8. The Kunitz-type inhibitor is eluted with 20 mM NH<sub>4</sub>HCO<sub>3</sub>, pH 7.8.

The Kunitz-type inhibitor is further purified and concentrated by chromatography on a Mono S column (Pharmacia-LKB Biotechnology AS, Alleroed, Denmark; 0.5 x 5 cm) equilibrated with 20 mM Bicine, pH 8.7. After washing with the equilibration buffer at 2 ml/min for 10 minutes, gradient elution of the Kunitz-type inhibitor is carried out over twelve minutes at 1 ml/min from 0 - 0.6 M NaCl in the equilibration buffer. Peak samples are pooled, and the Kunitz-type inhibitor is purified using reverse phase HPLC on a Vydac 214TP510 column (Mikro-lab, Aarhus, Denmark; 1.0 x 25 cm) with a gradient elution at 4 ml/min from 5% A (0.1% trifluoroacetic acid (TFA) in water) to 45% B (0.7% TFA in acetonitrile) in 20 minutes. The purified product is lyophilized in water, and inhibitor activity is measured.

Kunitz inhibitor activity is measured using the method essentially described by Norris et al. (ibid.). Briefly, various fixed concentrations of the Kunitz-type inhibitor are incubated in the presence of 0.24 µg/ml of porcine trypsin (Novo Nordisk A/S, Bagsvaerd, Denmark), 12.8 CU/l human plasmin (Kabi, Stockholm, Sweden) or 0.16 nkat/ml human plasma kallikrein (Kabi) in 100 mM NaCl, 50 mM Tris HCl, pH 7.4. After a 30 minute incubation the residual enzymatic activity is measured by the cleavage of a substrate solution containing 0.6 mM of either of the chromogenic peptidyl nitroanilide trypsin/plasmin substrates S2251 (D-Val-Leu-Lys-Nan; Kabi) or S2302 (D-Pro-Phe-Arg-Nan; Kabi) in assay buffer. The samples are incubated for 30 minutes after which the absorbance of each sample is measured at 405 nm. Plasmin or

trypsin activity is measured as a decrease in absorbance at 405 nm. From the results, the apparent inhibition constant  $K_i$  is calculated.

#### Example 4

##### 5 Effect of Recombinant zkun8 on the Amydolytic Activities of Human Thrombin, and Human Factor XA

###### A. Thrombin amidolytic activity assay

10 The ability of recombinant zkun8 to inhibit the amidolytic activity of human thrombin is determined by a colometric assay using human thrombin (prepared as described by Pedersen, et al., *J. Biol. Chem.* 265: 16786-16793, 1990; which is incorporated by reference herein in its entirety) and various concentrations of recombinant zkun8. The assay is set up in a microtiter plate format. Reactions of 200  $\mu$ l are prepared in the wells of the microtiter plate. The reaction mixtures contain  
15 various concentrations of recombinant zkun8 and 20 nM human thrombin in 50 mM Tris-HCl (pH 7.5), 0.1% BSA, 5 mM  $\text{CaCl}_2$ . The reactions are incubated at 37°C for 15 minutes. Following incubation, 50  $\mu$ l of 10 mM the chromogenic substrate S-2238 (H-D-Phe-Pip-Arg-p-nitroanilide, Chromogenix, AB, Mölndal, Sweden) is added to each well. The absorbance at 405 nm is determined in a kinetic microplate reader  
20 (Model UVMAX, Molecular Devices).

###### B. Human Factor Xa Amidolytic Assay

The ability of zkun8 to inhibit the amidolytic activity of factor Xa is determined by a colorimetric assay as described above using 20 nM human factor Xa  
25 (prepared as described by Kondo, and Kisiel, *Blood* 70, 1947-1954, 1987; which is incorporated by reference herein in its entirety) in place of the 20 nM human thrombin described above. The reactions are set up and incubated as described above replacing the human thrombin with human factor Xa. Following incubation, 50 ml of 10 mM of the chromogenic substrate S-2222 (Benzoyl-Ile-Glu-Gly-Arg-p-nitroanilide,  
30 Chromogenix, AB, Mölndal, Sweden) is added to each well. The absorbance at 405 nm is determined in a kinetic microplate reader (Model UVMAX, Molecular Devices).

#### Example 5

##### Expression of zkun8 in CHO cells

35 CHO DG44 cells (Chasin et al., *Som. Cell. Molec. Genet.* 12:555-666, 1986) are plated in 10-cm tissue culture dishes and allowed to grow to approximately 50% to 70% confluency overnight at 37°C, 5%  $\text{CO}_2$ , in Ham's F12/FBS media (Ham's

F12 medium (Life Technologies), 5% fetal bovine serum (Hyclone, Logan, UT), 1% L-glutamine (JRH Biosciences, Lenexa, KS), 1% sodium pyruvate (Life Technologies)). The cells are then transfected with the plasmid zkun8/pZMP6 by liposome-mediated transfection using a 3:1 (w/w) liposome formulation of the polycationic lipid 2,3-dioleoyloxy-N-[2(sperminecarboxamido)ethyl]-N,N-dimethyl-1-propaniminium-trifluoroacetate and the neutral lipid dioleoyl phosphatidylethanolamine in membrane-filtered water (Lipofectamine™ Reagent, Life Technologies), in serum free (SF) media formulation (Ham's F12, 10 mg/ml transferrin, 5 mg/ml insulin, 2 mg/ml fetuin, 1% L-glutamine and 1% sodium pyruvate). Zkun8/pZMP6 is diluted into 15-ml tubes to a total final volume of 640 µl with SF media. 35 µl of Lipofectamine™ is mixed with 605 µl of SF medium. The resulting mixture is added to the DNA mixture and allowed to incubate approximately 30 minutes at room temperature. Five ml of SF media is added to the DNA:Lipofectamine™ mixture. The cells are rinsed once with 5 ml of SF media, aspirated, and the DNA:Lipofectamine™ mixture is added. The cells are incubated at 37°C for five hours, then 6.4 ml of Ham's F12/10% FBS, 1% PSN media is added to each plate. The plates are incubated at 37°C overnight, and the DNA:Lipofectamine™ mixture is replaced with fresh 5% FBS/Ham's media the next day. On day 3 post-transfection, the cells are split into T-175 flasks in growth medium. On day 7 posttransfection, the cells are stained with FITC-anti-CD8 monoclonal antibody (Pharmingen, San Diego, CA) followed by anti-FITC-conjugated magnetic beads (Miltenyi Biotec). The CD8-positive cells are separated using commercially available columns (mini-MACS columns; Miltenyi Biotec) according to the manufacturer's directions and put into DMEM/Ham's F12/5% FBS without nucleosides but with 50 nM methotrexate (selection medium).

Cells are plated for subcloning at a density of 0.5, 1 and 5 cells per well in 96-well dishes in selection medium and allowed to grow out for approximately two weeks. The wells are checked for evaporation of medium and brought back to 200 µl per well as necessary during this process. When a large percentage of the colonies in the plate are near confluency, 100 µl of medium is collected from each well for analysis by dot blot, and the cells are fed with fresh selection medium. The supernatant is applied to a nitrocellulose filter in a dot blot apparatus, and the filter is treated at 100°C in a vacuum oven to denature the protein. The filter is incubated in 625 mM Tris-glycine, pH 9.1, 5mM β-mercaptoethanol, at 65°C, 10 minutes, then in 2.5% non-fat dry milk Western A Buffer (0.25% gelatin, 50 mM Tris-HCl pH 7.4, 150 mM NaCl, 5 mM EDTA, 0.05% Igepal CA-630) overnight at 4°C on a rotating shaker. The filter is incubated with the antibody-HRP conjugate in 2.5% non-fat dry milk Western A buffer for 1 hour at room temperature on a rotating shaker. The filter is then washed three

times at room temperature in PBS plus 0.01% Tween 20, 15 minutes per wash. The filter is developed with chemiluminescence reagents (ECL™ direct labelling kit; Amersham Corp., Arlington Heights, IL) according to the manufacturer's directions and exposed to film (Hyperfilm ECL, Amersham Corp.) for approximately 5 minutes.

5 Positive clones are trypsinized from the 96-well dish and transferred to 6-well dishes in selection medium for scaleup and analysis by Western blot.

#### Example 6

##### Expression of zkun8 in BHK cells

10 Full-length zkun8 protein is produced in BHK cells transfected with pZMP6/zkun8 (Example 1). BHK 570 cells (ATCC CRL-10314) are plated in 10-cm tissue culture dishes and allowed to grow to approximately 50 to 70% confluence overnight at 37°C, 5% CO<sub>2</sub>, in DMEM/FBS media (DMEM, Gibco/BRL High Glucose; Life Technologies), 5% fetal bovine serum (Hyclone, Logan, UT), 1 mM L-glutamine

15 (JRH Biosciences, Lenexa, KS), 1 mM sodium pyruvate (Life Technologies). The cells are then transfected with pZMP6/zkun8 by liposome-mediated transfection (using Lipofectamine™; Life Technologies), in serum free (SF) media (DMEM supplemented with 10 mg/ml transferrin, 5 mg/ml insulin, 2 mg/ml fetuin, 1% L-glutamine and 1% sodium pyruvate). The plasmid is diluted into 15-ml tubes to a total final volume of

20 640 µl with SF media. 35 µl of the lipid mixture is mixed with 605 µl of SF medium, and the resulting mixture is allowed to incubate approximately 30 minutes at room temperature. Five milliliters of SF media is then added to the DNA:lipid mixture. The cells are rinsed once with 5 ml of SF media, aspirated, and the DNA:lipid mixture is added. The cells are incubated at 37°C for five hours, then 6.4 ml of DMEM/10% FBS,

25 1% PSN media is added to each plate. The plates are incubated at 37°C overnight, and the DNA:lipid mixture is replaced with fresh 5% FBS/DMEM media the next day. On day 5 post-transfection, the cells are split into T-162 flasks in selection medium (DMEM + 5% FBS, 1% L-Gln, 1% NaPyr, 1 µM methotrexate). Approximately 10 days post-transfection, two 150-mm culture dishes of methotrexate-resistant colonies

30 from each transfection are trypsinized, and the cells are pooled and plated into a T-162 flask and transferred to large-scale culture.

#### Example 7

##### Expression of zkun8 in adenovirus

35 For construction of adenovirus vectors, the protein coding region of human zkun8 is amplified by PCR using primers that add PmeI and AscI restriction sites at the 5' and 3' termini respectively. Amplification is performed with a full-length

zkun8 cDNA template in a PCR reaction as follows: one cycle at 95°C for 5 minutes; followed by 15 cycles at 95°C for 1 min., 61°C for 1 min., and 72°C for 1.5 min.; followed by 72°C for 7 min.; followed by a 4°C soak. The PCR reaction product is loaded onto a 1.2% low-melting-temperature agarose gel in TAE buffer (0.04 M Tris-acetate, 0.001 M EDTA). The zkun8 PCR product is excised from the gel and purified using a commercially available kit comprising a silica gel membrane spin column (QIAquick® PCR Purification Kit and gel cleanup kit; Qiagen, Inc.) as per kit instructions. The PCR product is then digested with PmeI and AscI, phenol/chloroform extracted, EtOH precipitated, and rehydrated in 20 ml TE (Tris/EDTA pH 8). The zkun8 fragment is then ligated into the PmeI-AscI sites of the transgenic vector pTG12-8 and transformed into *E. coli* DH10B™ competent cells by electroporation. Vector pTG12-8 was derived from p2999B4 (Palmiter et al., *Mol. Cell Biol.* 13:5266-5275, 1993) by insertion of a rat insulin II intron (ca. 200 bp) and polylinker (Fse I/Pme I/Asc I) into the Nru I site. The vector comprises a mouse metallothionein (MT-1) promoter (ca. 750 bp) and human growth hormone (hGH) untranslated region and polyadenylation signal (ca. 650 bp) flanked by 10 kb of MT-1 5' flanking sequence and 7 kb of MT-1 3' flanking sequence. The cDNA is inserted between the insulin II and hGH sequences. Clones containing zkun8 are identified by plasmid DNA miniprep followed by digestion with PmeI and AscI. A positive clone is sequenced to insure that there were no deletions or other anomalies in the construct.

DNA is prepared using a commercially available kit (Maxi Kit, Qiagen, Inc.), and the zkun8 cDNA is released from the pTG12-8 vector using PmeI and AscI enzymes. The cDNA is isolated on a 1% low melting temperature agarose gel and excised from the gel. The gel slice is melted at 70°C, and the DNA is extracted twice with an equal volume of Tris-buffered phenol, precipitated with EtOH, and resuspended in 10 µl H<sub>2</sub>O.

The zkun8 cDNA is cloned into the EcoRV-AscI sites of a modified pAdTrack-CMV (He, T.-C. et al., *Proc. Natl. Acad. Sci. USA* 95:2509-2514, 1998). This construct contains the green fluorescent protein (GFP) marker gene. The CMV promoter driving GFP expression is replaced with the SV40 promoter, and the SV40 polyadenylation signal is replaced with the human growth hormone polyadenylation signal. In addition, the native polylinker is replaced with FseI, EcoRV, and AscI sites. This modified form of pAdTrack-CMV is named pZyTrack. Ligation is performed using a commercially available DNA ligation and screening kit (Fast-Link® kit; Epicentre Technologies, Madison, WI). Clones containing zalpha51 are identified by digestion of mini prep DNA with FseI and AscI. In order to linearize the plasmid, approximately 5 µg of the resulting pZyTrack zkun8 plasmid is digested with PmeI.



Approximately 1  $\mu$ g of the linearized plasmid is cotransformed with 200 ng of supercoiled pAdEasy (He et al., *ibid.*) into *E. coli* BJ5183 cells (He et al., *ibid.*). The co-transformation is done using a Bio-Rad Gene Pulser at 2.5 kV, 200 ohms and 25  $\mu$ Fa. The entire co-transformation mixture is plated on 4 LB plates containing 25  $\mu$ g/ml kanamycin. The smallest colonies are picked and expanded in LB/kanamycin, and recombinant adenovirus DNA is identified by standard DNA miniprep procedures. The recombinant adenovirus miniprep DNA is transformed into *E. coli* DH10B™ competent cells, and DNA is prepared using a Maxi Kit (Qiagen, Inc.) according to kit instructions.

Approximately 5  $\mu$ g of recombinant adenoviral DNA is digested with PacI enzyme (New England Biolabs) for 3 hours at 37°C in a reaction volume of 100  $\mu$ l containing 20-30U of PacI. The digested DNA is extracted twice with an equal volume of phenol/chloroform and precipitated with ethanol. The DNA pellet is resuspended in 10  $\mu$ l distilled water. A T25 flask of QBI-293A cells (Quantum Biotechnologies, Inc. Montreal, Qc. Canada), inoculated the day before and grown to 60-70% confluence, is transfected with the PacI digested DNA. The PacI-digested DNA is diluted up to a total volume of 50  $\mu$ l with sterile HBS (150mM NaCl, 20mM HEPES). In a separate tube, 20  $\mu$ l of 1mg/ml N-[1-(2,3-Dioleoyloxy)propyl]-N,N,N-trimethyl-ammonium salts (DOTAP) (Boehringer Mannheim, Indianapolis, IN) is diluted to a total volume of 100  $\mu$ l with HBS. The DNA is added to the DOTAP, mixed gently by pipeting up and down, and left at room temperature for 15 minutes. The media is removed from the 293A cells and washed with 5 ml serum-free minimum essential medium (MEM) alpha containing 1mM sodium pyruvate, 0.1 mM MEM non-essential amino acids, and 25mM HEPES buffer (reagents obtained from Life Technologies, Gaithersburg, MD). 5 ml of serum-free MEM is added to the 293A cells and held at 37°C. The DNA/lipid mixture is added drop-wise to the T25 flask of 293A cells, mixed gently, and incubated at 37°C for 4 hours. After 4 hours the media containing the DNA/lipid mixture is aspirated off and replaced with 5 ml complete MEM containing 5% fetal bovine serum. The transfected cells are monitored for GFP expression and formation of foci (viral plaques).

Seven days after transfection of 293A cells with the recombinant adenoviral DNA, the cells express the GFP protein and start to form foci (viral "plaques"). The crude viral lysate is collected using a cell scraper to collect all of the 293A cells. The lysate is transferred to a 50-ml conical tube. To release most of the virus particles from the cells, three freeze/thaw cycles are done in a dry ice/ethanol bath and a 37°C waterbath.

The crude lysate is amplified (Primary (1°) amplification) to obtain a working "stock" of zkun8 rAdV lysate. Ten 10cm plates of nearly confluent (80-90%) 293A cells are set up 20 hours previously, 200 ml of crude rAdV lysate is added to each 10-cm plate, and the cells are monitored for 48 to 72 hours for CPE (cytopathic effect) under the white light microscope and expression of GFP under the fluorescent microscope. When all of the 293A cells show CPE, this stock lysate is collected and freeze/thaw cycles performed as described above.

A secondary (2°) amplification of zkun8 rAdV is then performed. Twenty 15-cm tissue culture dishes of 293A cells are prepared so that the cells are 80-90% confluent. All but 20 ml of 5% MEM media is removed, and each dish is inoculated with 300-500 ml of the 1° amplified rAdV lysate. After 48 hours the 293A cells are lysed from virus production, the lysate is collected into 250-ml polypropylene centrifuge bottles, and the rAdV is purified.

NP-40 detergent is added to a final concentration of 0.5% to the bottles of crude lysate in order to lyse all cells. Bottles are placed on a rotating platform for 10 minutes agitating as fast as possible without the bottles falling over. The debris is pelleted by centrifugation at 20,000 X G for 15 minutes. The supernatant is transferred to 250-ml polycarbonate centrifuge bottles, and 0.5 volume of 20% PEG8000/2.5 M NaCl solution is added. The bottles are shaken overnight on ice. The bottles are centrifuged at 20,000 X G for 15 minutes, and the supernatant is discarded into a bleach solution. Using a sterile cell scraper, the white, virus/PEG precipitate from 2 bottles is resuspended in 2.5 ml PBS. The resulting virus solution is placed in 2-ml microcentrifuge tubes and centrifuged at 14,000 X G in the microcentrifuge for 10 minutes to remove any additional cell debris. The supernatant from the 2-ml microcentrifuge tubes is transferred into a 15-ml polypropylene snapcap tube and adjusted to a density of 1.34 g/ml with CsCl. The solution is transferred to 3.2-ml, polycarbonate, thick-walled centrifuge tubes and spun at 348,000 X G for 3-4 hours at 25°C. The virus forms a white band. Using wide-bore pipette tips, the virus band is collected.

A commercially available ion-exchange columns (e.g., PD-10 columns prepacked with Sephadex® G-25M; Pharmacia Biotech, Piscataway, NJ) is used to desalt the virus preparation. The column is equilibrated with 20 ml of PBS. The virus is loaded and allowed to run into the column. 5 ml of PBS is added to the column, and fractions of 8-10 drops are collected. The optical densities of 1:50 dilutions of each fraction are determined at 260 nm on a spectrophotometer. Peak fractions are pooled, and the optical density (OD) of a 1:25 dilution is determined. OD is converted to virus concentration using the formula:  $(OD \text{ at } 260\text{nm})(25)(1.1 \times 10^{12}) = \text{virions/ml}$ .

To store the virus, glycerol is added to the purified virus to a final concentration of 15%, mixed gently but effectively, and stored in aliquots at -80°C.

A protocol developed by Quantum Biotechnologies, Inc. (Montreal, Canada) is followed to measure recombinant virus infectivity. Briefly, two 96-well  
5 tissue culture plates are seeded with  $1 \times 10^4$  293A cells per well in MEM containing 2% fetal bovine serum for each recombinant virus to be assayed. After 24 hours 10-fold dilutions of each virus from  $1 \times 10^{-2}$  to  $1 \times 10^{-14}$  are made in MEM containing 2% fetal bovine serum. 100 µl of each dilution is placed in each of 20 wells. After 5 days at 37°C, wells are read either positive or negative for CPE, and a value for "Plaque  
10 Forming Units/ml" (PFU) is calculated.

#### Example 8

##### Expression of zkun8

A panel of cDNAs from human tissues is screened for zkun8 expression  
15 using PCR. The panel is made in-house and contained 94 marathon cDNA and cDNA samples from various normal and cancerous human tissues and cell lines is shown in Table 4, below. The cDNAs come from in-house libraries or marathon cDNAs from in-house RNA preps, Clontech RNA, or Invitrogen RNA. The marathon cDNAs are made using the marathon-Ready™ kit (Clontech, Palo Alto, CA) and QC tested with clathrin  
20 primers, and then diluted based on the intensity of the clathrin band. To assure quality of the panel samples, three tests for quality control (QC) are run: (1) To assess the RNA quality used for the libraries, the in-house cDNAs are tested for average insert size by PCR with vector oligonucleotides that are specific for the vector sequences for an individual cDNA library; (2) Standardization of the concentration of the cDNA in  
25 panel samples is achieved using standard PCR methods to amplify full length alpha tubulin or G3PDH cDNA using a 5' vector oligonucleotide and 3' alpha tubulin specific oligonucleotide primer or 3' G3PDH specific oligo primer; and (3) a sample is sequenced to check for possible ribosomal or mitochondrial DNA contamination. The

- electrophoresis using a 4% agarose gel. The correct predicted DNA fragment size is observed in: (1) fetal tissues from liver, brain, heart, kidney, lung, muscle and skin; (2) normal tissues from adrenal gland, bladder, bone marrow, brain, cervix, colon, liver, lung, lymph node, mammary gland, ovary, pituitary, prostate, rectum, salivary gland, skeletal muscle, small intestine, spinal cord, stomach, testis, thymus, trachea, and uterus; and (3) cancerous tissues from liver, ovary, rectum, stomach and uterus.

Table 4

Tissue/Cell line	#samples	Tissue/Cell line	#samples
Adrenal gland	1	Bone marrow	3
Bladder	1	Fetal brain	3
Bone Marrow	1	Islet	2
Brain	1	Prostate	3
Cervix	1	RPMI #1788 (ATCC # CCL-156)	2
Colon	1	Testis	4
Fetal brain	1	Thyroid	2
Fetal heart	1	WI38 (ATCC # CCL-75)	2
Fetal kidney	1	ARIP (ATCC # CRL-1674 - rat)	1
Fetal liver	1	HaCat - human keratinocytes	1
Fetal lung	1	HPV (ATCC # CRL-2221)	1
Fetal muscle	1	Adrenal gland	1
Fetal skin	1	Prostate SM	2
Heart	2	CD3+ selected PBMC's Ionomycin + PMA stimulated	1
K562 (ATCC # CCL-243)	1	HPVS (ATCC # CRL-2221) - selected	1
Kidney	1	Heart	1
Liver	1	Pituitary	1
Lung	1	Placenta	2
Lymph node	1	Salivary gland	1
Melanoma	1	HL60 (ATCC # CCL-240)	3

Pancreas	1	Platelet	1
Pituitary	1	HBL-100	1
Placenta	1	Renal mesangial	1
Prostate	1	T-cell	1
Rectum	1	Neutrophil	1
Salivary Gland	1	MPC	1
Skeletal muscle	1	Hut-102 (ATCC # TIB-162)	1
Small intestine	1	Endothelial	1
Spinal cord	1	HepG2 (ATCC # HB-8065)	1
Spleen	1	Fibroblast	1
Stomach	1	E. Histo	1
Testis	2		
Thymus	1		
Thyroid	1		
Trachea	1		
Uterus	1		
Esophagus tumor	1		
Gastric tumor	1		
Kidney tumor	1		
Liver tumor	1		
Lung tumor	1		
Ovarian tumor	1		
Rectal tumor	1		
Uterus tumor	1		

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

## CLAIMS

What is claimed:

1. An isolated polypeptide comprising a sequence of amino acid residues that is at least 90% identical to a sequence selected from the group consisting of:

(a) a sequence of amino acid residues as shown in SEQ ID NO: 2 from residue 328 to residue 378; and

(b) a sequence of amino acid residues as shown in SEQ ID NO: 2 from residue 386 to residue 436.

2. The isolated polypeptide of claim 1, wherein the sequence of amino acid residues is identical to residues 324 to 381 of SEQ ID NO: 2.

3. The isolated polypeptide of claim 1, wherein the sequence of amino acid residues is identical to residues 382 to 440 of SEQ ID NO: 2.

4. An isolated polypeptide comprising a sequence of amino acid residues selected from the group consisting of:

(a) a sequence of amino acid residues as shown in SEQ ID NO: 4 from residue 1 to residue 51; and

(b) a sequence of amino acid residues as shown in SEQ ID NO: 5 from residue 1 to residue 51.

5. An isolated protein comprising:

a first kunitz domain polypeptide that is at least 90% identical to the sequence of amino acid residues as shown in SEQ ID NO: 2 from residue 324 to residue 381; and

a second kunitz domain polypeptide that is at least 90% identical to the sequence of amino acid residues as shown in SEQ ID NO: 2 from residue 382 to residue 440.

6. The isolated protein of claim 5, wherein the first kunitz domain polypeptide is the sequence as shown in SEQ ID NO: 2 from residue 324 to residue 381 and the second kunitz domain polypeptide is the sequence as shown in SEQ ID NO: 2 from residue 382 to residue 440.

7. An isolated protein comprising:

a first kunitz domain polypeptide as shown in SEQ ID NO: 4; and

a second kunitz domain polypeptide as shown in SEQ ID NO: 5.

8. An isolated polypeptide comprising a sequence of amino acid residues that is at least 90% identical to the sequence as shown in SEQ ID NO: 2 from residue 35 to residue 576.

9. The isolated polypeptide of claim 8, wherein the sequence of amino acid residues is the sequence as shown in SEQ ID NO: 2 from residue 35 to residue 576.

10. An isolated polypeptide comprising a sequence of amino acid residues shown in SEQ ID NO: 2 from amino acid residue 1 to amino acid residue 576.

11. An isolated polypeptide comprising a sequence of amino acid residues selected from the group consisting of:

- (a) amino acid residues 1-34 of SEQ ID NO: 2;
- (b) amino acid residues 35-98 of SEQ ID NO: 2;
- (c) amino residues 101-180 of SEQ ID NO: 2;
- (d) amino acid residues 227-310 of SEQ ID NO: 2;
- (e) amino acid residues 324-384 of SEQ ID NO: 2;
- (f) amino acid residues 382-440 of SEQ ID NO: 2; and
- (g) amino acid residues 441-576 of SEQ ID NO: 2.

12. An isolated polynucleotide molecule comprising a sequence of nucleotides selected from the group consisting of:

- (a) a polynucleotide molecule encoding a polypeptide that is at least 90% identical to the sequence shown in SEQ ID NO: 2 from residue 328 to residue 378; and
- (b) a polynucleotide molecule encoding a polypeptide that is at least 90% identical to the sequence shown in SEQ ID NO: 2 from residue 386 to residue 436.

13. An isolated polynucleotide molecule comprising a sequence of nucleotides selected from the group consisting of:

- (a) a polynucleotide molecule encoding a polypeptide that is at least 90% identical to the sequence shown in SEQ ID NO: 2 from residue 324 to residue 381; and
- (b) a polynucleotide molecule encoding a polypeptide that is at least 90% identical to the sequence shown in SEQ ID NO: 2 from residue 382 to residue 440.

14. The isolated polynucleotide molecule of claim 13, wherein the sequence of polynucleotides encodes a polypeptide that is identical to residues 324 to 381 or residues 382 to 440 of SEQ ID NO: 2.

15. An isolated polynucleotide molecule comprising a sequence of nucleotides that encodes a polypeptide as shown in SEQ ID NO: 4 from residue 1 to residue 51 or a polypeptide as shown in SEQ ID NO: 5 from residue 1 to residue 51.

16. An isolated polynucleotide molecule comprising a sequence of nucleotides that encodes a polypeptide comprising:

a first kunitz domain polypeptide that is at least 90% identical to the sequence of amino acid residues as shown in SEQ ID NO: 2 from residue 324 to residue 381; and

a second kunitz domain polypeptide that is at least 90% identical to the sequence of amino acid residues as shown in SEQ ID NO: 2 from residue 382 to residue 440.

17. The isolated polynucleotide molecule of claim 16, wherein the first kunitz domain polypeptide is the sequence as shown in SEQ ID NO: 2 from residue 324 to residue 381 and the second kunitz domain polypeptide is the sequence as shown in SEQ ID NO: 2 from residue 382 to residue 440.

18. An isolated polynucleotide molecule comprising a sequence of nucleotides that encode a polypeptide comprising:

a first kunitz domain polypeptide as shown in SEQ ID NO: 4; and

a second kunitz domain polypeptide as shown in SEQ ID NO: 5.

19. An isolated polynucleotide molecule comprising a sequence of nucleotides that encodes a polypeptide that is at least 90% identical to the sequence as shown in SEQ ID NO: 2 from residue 35 to residue 576.

20. The isolated polynucleotide of claim 19, wherein the sequence of nucleotides encode a polypeptide that is the sequence as shown in SEQ ID NO: 2 from residue 1 to residue 576.

21. An isolated polynucleotide encoding for a polypeptide comprising a sequence of amino acid residues selected from the group consisting of:

(a) amino acid residues 1-34 of SEQ ID NO: 2;



- (b) amino acid residues 35-98 of SEQ ID NO: 2;
- (c) amino residues 101-180 of SEQ ID NO: 2;
- (d) amino acid residues 227-310 of SEQ ID NO: 2;
- (e) amino acid residues 324-384 of SEQ ID NO: 2;
- (f) amino acid residues 382-440 of SEQ ID NO: 2; and
- (g) amino acid residues 441-576 of SEQ ID NO: 2.

22. An expression vector comprising the following operably linked elements:

- (a) a transcription promoter;
- (b) a polynucleotide molecule according to any one of claims 13, 15 or 17; and
- (c) a transcription terminator.

23. The expression vector of claim 21 further comprising a secretory signal sequence operably linked to the polynucleotide molecule.

24. A cultured cell comprising the expression vector of claim 21.

25. A method of producing a polypeptide comprising:  
culturing a cell according to claim 24 under conditions wherein the polynucleotide molecule is expressed; and  
recovering the protein encoded by the polynucleotide.

26. An antibody that specifically binds to the protein of claim 1 or claim 11.

27. An antibody that specifically binds to the protein of claim 10.

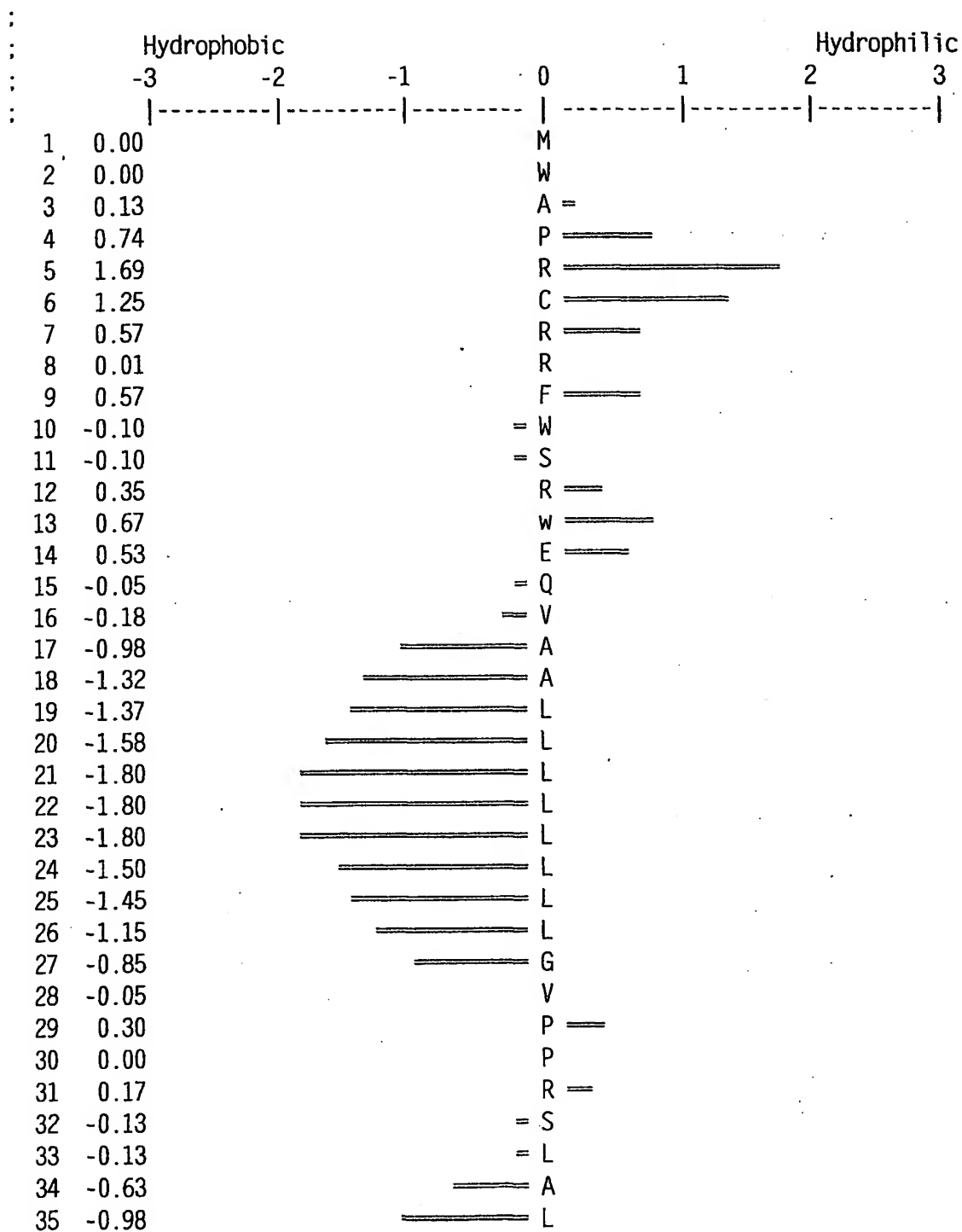
28. A fusion protein comprising at least two polypeptides, wherein a first polypeptide and second polypeptide, and wherein at least one of the polypeptides comprise a sequence of amino acid residues as shown in SEQ ID NO: 2 from amino acid residue 324 to amino acid residue 381 or as shown in SEQ ID NO: 2 from amino acid residue 382 to amino acid residue 440.

29. A method of inhibiting protease degradation or activity in a composition containing plasma proteins comprising adding a zkun8 polypeptide composition

comprising a sequence of amino acid residues as shown in SEQ ID NO: 2 from amino acid residue 324 to amino acid residue 381 or as shown in SEQ ID NO: 2 from amino acid residue 382 to amino acid residue 440 to the composition containing plasma proteins in an amount sufficient to reduce degradation of the composition by proteases or protease activity in the composition.

30. The method of claim 29, wherein reduction of degradation or activity is determined by chromogenic substrate assays or clotting time assays.

1/15



2/15

36 -0.18  
37 -0.48  
38 -0.13  
39 -0.22  
40 -0.30  
41 0.00  
42 -0.80  
43 -0.58  
44 -0.63  
45 -0.52  
46 0.07  
47 -0.15  
48 0.18  
49 0.35  
50 0.38  
51 0.05  
52 -1.02  
53 -1.05  
54 -0.58  
55 -0.67  
56 -0.67  
57 -0.32  
58 0.18  
59 0.27  
60 0.27  
61 0.85  
62 1.32  
63 1.10  
64 1.67  
65 1.77  
66 1.77  
67 1.30  
68 1.30  
69 1.30  
70 1.30  
71 1.30  
72 0.82  
73 1.28  
74 1.28

= P  
== P  
= I  
= R  
== Y  
S  
== H  
== A  
== G  
== I  
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3/15

75	1.28	y	=====
76	0.62	E	=====
77	0.68	K	=====
78	0.70	C	=====
79	-0.05	C	
80	-0.72	P	=====
81	-0.55	N	=====
82	-0.45	V	=====
83	0.05	C	
84	0.07	G	=
85	0.15	T	=====
86	0.07	K	=
87	-0.02	S	
88	-0.03	C	
89	-0.03	V	
90	-0.47	A	=====
91	-0.52	A	=====
92	0.23	R	=====
93	0.07	Y	=
94	0.65	M	=====
95	0.15	D	=====
96	1.03	V	=====
97	1.75	K	=====
98	1.25	G	=====
99	1.50	K	=====
100	0.75	K	=====
101	0.75	G	=====
102	0.03	P	
103	-0.47	V	=====
104	0.03	G	
105	0.53	M	=====
106	0.70	P	=====
107	0.63	K	=====
108	0.68	E	=====
109	1.18	A	=====
110	0.60	T	=====
111	-0.32	C	=====
112	-0.45	D	=====
113	-0.55	H	=====

4/15

114	-0.68	=====	F
115	-1.15	=====	M
116	-1.03	=====	C
117	-0.62	=====	L
118	-0.35	=====	Q
119	0.32	=====	Q =
120	0.45	=====	G =
121	0.92	=====	S =
122	0.58	=====	E =
123	0.02	=====	C
124	0.47	=====	D =
125	-0.03	=====	I
126	0.17	=====	W =
127	-0.33	=====	D
128	-0.28	=====	G
129	0.12	=====	Q =
130	0.12	=====	P =
131	-0.05	=====	V
132	0.42	=====	C =
133	0.92	=====	K =
134	1.67	=====	C =
135	1.67	=====	K =
136	1.67	=====	D =
137	2.33	=====	R =
138	2.33	=====	C =
139	1.83	=====	E =
140	1.38	=====	K =
141	1.13	=====	E =
142	0.07	=====	P =
143	-0.60	=====	S
144	-1.18	=====	F
145	-1.13	=====	t
146	-0.68	=====	C
147	-0.27	=====	A
148	0.00	=====	S
149	0.10	=====	D =
150	-0.20	=====	G
151	-0.63	=====	L
152	-1.10	=====	T

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153	-0.60	=====	Y
154	-0.47	=====	Y
155	-0.78	=====	N
156	-0.62	=====	R
157	0.27		C ==
158	0.15		Y =
159	0.15		M =
160	0.23		D =
161	0.45		A ==
162	0.72		E =====
163	0.72		A =====
164	0.80		C =====
165	0.00		S
166	-0.48	=====	K
167	-0.62	=====	G
168	-0.75	=====	I
169	-1.50	=====	t
170	-1.75	=====	L
171	-1.52	=====	A
172	-1.12	=====	V
173	-0.32	=====	V
174	-0.62	=====	T
175	-0.45	=====	C
176	-0.62	=====	R
177	-0.62	=====	Y
178	-1.02	=====	H
179	-1.52	=====	F
180	-1.10	=====	T
181	-1.08	=====	W
182	-0.62	=====	P
183	-0.55	=====	N
184	0.02		T
185	0.02		S
186	-0.02		P
187	0.55		P =====
188	0.43		P =====
189	0.37		P =====
190	0.15		E =
191	0.07		T =

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192	0.07		T =
193	-0.50	=====	M
194	-0.50	=====	H
195	-0.52	=====	P
196	-0.25	=====	T
197	-0.17	=====	T
198	0.33		A =====
199	0.33		S =====
200	0.40		P =====
201	0.98		E =====
202	0.63		T =====
203	1.13		P =====
204	0.42		E =====
205	0.40		L =====
206	0.32		D =====
207	-0.18		= M
208	0.03		A
209	-0.77	=====	A
210	-0.85	=====	P
211	-0.73	=====	A
212	-0.62	=====	L
213	-0.62	=====	L
214	-0.78	=====	N
215	-0.57	=====	N
216	-0.23	=====	P
217	-0.22	=====	V
218	-0.50	=====	H
219	-1.07	=====	Q
220	-1.03	=====	S
221	-0.95	=====	V
222	-0.48	=====	t
223	-0.60	=====	M
224	-0.60	=====	G
225	-0.60	=====	E
226	-0.80	=====	T
227	-1.10	=====	V
228	-1.77	=====	S
229	-1.20	=====	F
230	-1.20	=====	L



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231	-0.88	=====	C
232	-0.47	=====	D
233	0.33		V ==
234	0.50		V =====
235	0.50		G =====
236	0.75		R =====
237	1.50		P =====
238	1.20		R =====
239	0.63		P =====
240	0.07		E =
241	0.07		I =
242	0.57		T =====
243	0.10		W =
244	0.10		E =
245	0.67		K =====
246	1.73		Q =====
247	1.73		L =====
248	1.73		E =====
249	1.73		D =====
250	1.78		R =====
251	1.03		E =====
252	0.32		N ==
253	0.32		V ==
254	-0.18	=====	V
255	-0.18	=====	M
256	-0.02		R
257	-0.02		P
258	0.70		N =====
259	0.20		H ==
260	0.23		V ==
261	-0.05		R
262	-0.22	=====	G
263	-0.22	=====	N
264	-0.78	=====	V
265	-0.75	=====	V
266	-1.08	=====	V
267	-0.92	=====	T
268	-0.63	=====	N
269	-0.68	=====	I

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270	-0.87	=====	A
271	-1.20	=====	Q
272	-1.28	=====	L
273	-1.17	=====	V
274	-1.28	=====	I
275	-0.95	=====	Y
276	-1.00	=====	N
277	-0.67	=====	A
278	0.22		Q =
279	0.10		L =
280	0.18		Q =
281	-0.15		= D
282	-0.23		= A
283	-0.33		= G
284	-1.00	=====	I
285	-0.98	=====	Y
286	-1.07	=====	T
287	-0.27	=====	C
288	0.15		T =
289	-0.03		A
290	0.05		R
291	-0.45	=====	N
292	-0.62	=====	V
293	-1.42	=====	A
294	-0.95	=====	g
295	-0.78	=====	V
296	-0.20	=====	L
297	-0.05		R
298	0.20		A =
299	0.20		D =
300	-0.25	=====	F
301	-0.42	=====	P
302	-1.17	=====	L
303	-0.25	=====	S
304	-0.25	=====	V
305	0.37		V =
306	0.35		R =
307	0.52		G =
308	0.68		h =

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309 0.10  
310 0.03  
311 -0.23  
312 0.23  
313 0.37  
314 0.50  
315 0.58  
316 0.68  
317 0.63  
318 0.07  
319 -0.07  
320 -0.53  
321 -0.53  
322 -0.65  
323 -0.73  
324 -0.17  
325 -0.25  
326 -0.13  
327 0.37  
328 0.45  
329 0.53  
330 0.53  
331 0.75  
332 1.55  
333 1.55  
334 1.38  
335 1.38  
336 1.38  
337 1.83  
338 1.37  
339 0.80  
340 1.47  
341 1.30  
342 0.72  
343 -0.20  
344 0.27  
345 0.25  
346 -0.22  
347 -0.13

Q =  
A  
= A  
A =  
T ==  
S ==  
E ==  
S ==  
S ==  
P =  
= N  
== G  
== T  
== A  
== F  
= P  
= A  
= A  
E ==  
C ==  
L ==  
K ==  
P ==  
P ==  
D ==  
S ==  
E ==  
D ==  
C ==  
G ==  
E ==  
E ==  
Q ==  
T ==  
= R  
W ==  
H ==  
= F  
= D

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348	-0.02	A
349	0.43	Q ==
350	-0.23	= A
351	-0.45	= N
352	-1.05	= N
353	-1.38	= C
354	-1.48	= L
355	-1.93	= t
356	-1.77	= F
357	-1.55	= T
358	-1.15	= F
359	-0.82	= G
360	-0.25	= H
361	0.20	C =
362	-0.10	= H
363	0.02	R
364	0.10	N =
365	-0.23	= L
366	-0.23	= N
367	-0.33	= H
368	-0.02	F
369	0.45	E ==
370	0.45	T ==
371	0.70	Y ==
372	-0.02	E
373	-0.25	= A
374	-0.35	= C
375	-1.02	= M
376	-1.15	= L
377	-0.93	= A
378	-0.72	= C
379	-0.42	= M
380	-0.63	= S
381	-0.55	= G
382	-0.42	= P
383	-0.63	= L
384	-0.58	= A
385	-0.88	= A
386	-0.58	= C

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387	-0.58	=====	S
388	-0.80	=====	L
389	-0.60	=====	P
390	-0.65	=====	A
391	-0.35	=====	L
392	-0.52	=====	Q
393	0.07		G =
394	0.28		P ==
395	-0.13		= C
396	-0.22		= K
397	-0.22		= A
398	0.45		Y =====
399	-0.62	=====	A
400	-0.62	=====	P
401	-0.62	=====	R
402	-0.50	=====	W
403	-0.45	=====	A
404	-0.92	=====	Y
405	-0.42	=====	N
406	-0.33	=====	S
407	0.08		Q =
408	-0.12		= T
409	-0.13		= G
410	-0.12		= Q
411	-0.47	=====	C
412	-0.72	=====	Q
413	-1.13	=====	S
414	-0.97	=====	F
415	-1.00	=====	V
416	-1.22	=====	Y
417	-0.30	=====	G
418	-0.05		G
419	0.37		C ==
420	0.37		E ==
421	0.40		G ==
422	0.60		N =====
423	-0.32	=====	G
424	0.18		N =
425	0.20		N =

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426 0.70  
427 1.17  
428 1.05  
429 1.30  
430 1.30  
431 1.75  
432 1.30  
433 0.63  
434 0.72  
435 0.47  
436 -0.03  
437 -0.03  
438 -0.08  
439 0.12  
440 0.15  
441 1.07  
442 0.90  
443 0.90  
444 0.82  
445 0.62  
446 1.08  
447 0.58  
448 1.25  
449 0.78  
450 1.37  
451 1.23  
452 0.48  
453 -0.08  
454 -0.53  
455 -0.98  
456 -1.65  
457 -0.85  
458 -0.55  
459 0.52  
460 0.05  
461 0.22  
462 0.08  
463 -0.72  
464 -0.77

F  
E  
S  
R  
E  
A  
C  
E  
E  
S  
C  
P  
= F  
P =  
R =  
G  
N  
Q  
R  
C  
R  
A  
C  
K  
P  
R  
Q  
= K  
L  
V  
t  
S  
F  
C  
R  
S =  
D =  
F  
V

*13/15*

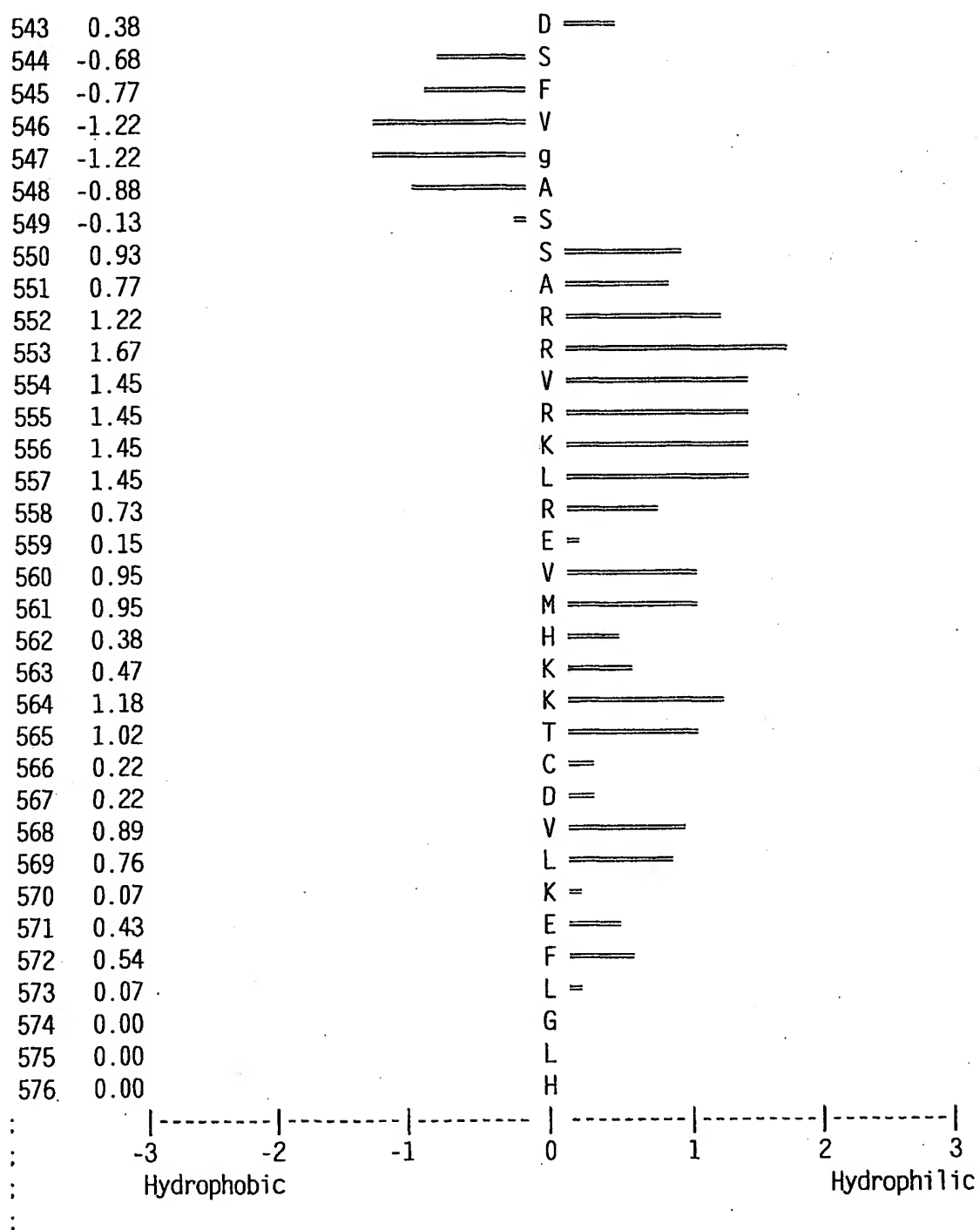
465	-0.77	=====	I
466	-0.60	=====	L
467	-0.30	=====	G
468	0.50		R =====
469	0.50		V =====
470	0.43		S =====
471	0.43		E =====
472	1.18		L =====
473	1.13		T =====
474	1.13		E =====
475	1.48		E =====
476	1.55		P =====
477	1.55		D =====
478	0.97		S =====
479	0.67		G =====
480	-0.08		= R
481	-0.20		= A
482	-0.45	=====	L
483	-0.45	=====	V
484	0.13		T =
485	0.18		V =
486	0.13		D =
487	0.70		E =====
488	1.45		V =====
489	1.45		L =====
490	1.45		K =====
491	1.48		D =====
492	1.78		E =====
493	0.98		K =====
494	0.98		M =====
495	0.07		G =
496	-0.73	=====	L
497	-0.52	=====	K
498	-0.48	=====	F
499	0.32		L =====
500	-0.18		= G
501	-0.07		= Q
502	0.73		E =====
503	0.48		P =====

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504	0.38	L	==
505	-0.42	E	==
506	-0.72	V	==
507	-0.50	T	==
508	-1.25	L	==
509	-0.50	L	==
510	-1.00	H	==
511	-0.78	V	==
512	-0.65	D	==
513	-0.57	W	==
514	-0.48	A	==
515	-0.98	C	==
516	-0.38	P	==
517	-0.55	C	==
518	-0.45	P	==
519	-0.70	N	==
520	-0.48	V	==
521	0.02	T	==
522	-0.23	V	==
523	0.02	S	==
524	-0.22	E	==
525	-0.27	M	==
526	-0.62	P	==
527	-1.33	L	==
528	-1.12	I	==
529	-0.62	I	==
530	-0.57	M	==
531	0.23	G	==
532	0.53	E	==
533	0.75	V	==
534	0.53	D	==
535	-0.05	G	==
536	-0.02	G	==
537	-0.82	M	==
538	-0.32	A	==
539	-0.32	M	==
540	0.40	L	==
541	0.53	R	==
542	0.33	P	==



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FIGURE

## SEQUENCE LISTING

&lt;110&gt; ZymoGenetics, Inc.

&lt;120&gt; KUNITZ DOMAIN POLYPEPTIDE ZKUN8

&lt;130&gt; 00-01PC

&lt;150&gt; US 09/515,225

&lt;151&gt; 2000-02-29

&lt;160&gt; 7

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 3301

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (237)...(1967)

&lt;400&gt; 1

ctcaggagag	ggagcttcct	tctaaagacc	tttcttttat	ctgaagccgc	acagcccggc	60
aggctgtgct	gacttggtgg	aggcagcagc	ggcagagcag	cctgagcagc	agcctgagca	120
ggaaacctgc	tggggtgggg	agggcagggtg	tctgcagccc	ctgagaagaa	ggccctggtg	180
ggccccagac	cctggcatcg	tttcagggga	ggtctctagc	cgccccagcc	tgcacc atg	239
				Met		
				1		

tgg gcc cca	agg tgt cgc	cgg ttc	tgg tct cgc	tgg gag cag	gtg gca	287
Trp Ala Pro	Arg Cys Arg	Arg Phe Trp	Ser Arg Trp	Glu Gln Val	Ala	
	5		10		15	

gcg ctg ctg	ctg ctg ctg	cta ctg ctc	ggg gtg ccc	ccg cga agc	ctg	335
Ala Leu Leu	Leu Leu Leu	Leu Leu Leu	Gly Val Pro	Pro Arg Ser	Leu	
	20		25		30	

gcg ctg ccg ccc atc cgc tat tcc cat gcc ggc atc tgc ccc aac gac Ala Leu Pro Pro Ile Arg Tyr Ser His Ala Gly Ile Cys Pro Asn Asp 35 40 45	383
atg aat ccc aac ctc tgg gtg gac gca cag agc acc tgc agg cgg gag Met Asn Pro Asn Leu Trp Val Asp Ala Gln Ser Thr Cys Arg Arg Glu 50 55 60 65	431
tgt gag acg gac cag gag tgt gag acc tat gag aag tgc tgc ccc aac Cys Glu Thr Asp Gln Glu Cys Glu Thr Tyr Glu Lys Cys Cys Pro Asn 70 75 80	479
gta tgt ggg acc aag agc tgc gtg gcg gcc cgc tac atg gac gtg aaa Val Cys Gly Thr Lys Ser Cys Val Ala Ala Arg Tyr Met Asp Val Lys 85 90 95	527
ggg aag aag ggc cca gtg ggc atg ccc aag gag gcc aca tgt gac cac Gly Lys Lys Gly Pro Val Gly Met Pro Lys Glu Ala Thr Cys Asp His 100 105 110	575
ttc atg tgt ctg cag cag ggc tct gag tgt gac atc tgg gat ggc cag Phe Met Cys Leu Gln Gln Gly Ser Glu Cys Asp Ile Trp Asp Gly Gln 115 120 125	623
ccc gtg tgt aag tgc aaa gac cgc tgt gag aag gag ccc agc ttt acc Pro Val Cys Lys Cys Lys Asp Arg Cys Glu Lys Glu Pro Ser Phe Thr 130 135 140 145	671
tgc gcc tcg gac ggc ctc acc tac tat aac cgc tgc tac atg gat gcc Cys Ala Ser Asp Gly Leu Thr Tyr Tyr Asn Arg Cys Tyr Met Asp Ala 150 155 160	719
gag gcc tgc tcc aaa ggc atc aca ctg gcc gtt gta acc tgc cgc tat Glu Ala Cys Ser Lys Gly Ile Thr Leu Ala Val Val Thr Cys Arg Tyr 165 170 175	767
cac ttc acc tgg ccc aac acc agc ccc cca cca cct gag acc acc atg His Phe Thr Trp Pro Asn Thr Ser Pro Pro Pro Pro Glu Thr Thr Met 180 185 190	815
cac ccc acc aca gcc tcc cca gag acc cct gag ctg gac atg gcg gcc His Pro Thr Thr Ala Ser Pro Glu Thr Pro Glu Leu Asp Met Ala Ala 195 200 205	863

cct gcg ctg ctc aac aac cct gtg cac cag tcg gtc acc atg ggt gag	911
Pro Ala Leu Leu Asn Asn Pro Val His Gln Ser Val Thr Met Gly Glu	
210 215 220 225	
aca gtg agc ttc ctc tgt gat gtg gtg ggc cgg ccc cgg cct gag atc	959
Thr Val Ser Phe Leu Cys Asp Val Val Gly Arg Pro Arg Pro Glu Ile	
230 235 240	
acc tgg gag aag cag ttg gag gat cgg gag aat gtg gtc atg cgg ccc	1007
Thr Trp Glu Lys Gln Leu Glu Asp Arg Glu Asn Val Val Met Arg Pro	
245 250 255	
aac cat gtg cgt ggc aac gtg gtg gtc acc aac att gcc cag ctg gtc	1055
Asn His Val Arg Gly Asn Val Val Val Thr Asn Ile Ala Gln Leu Val	
260 265 270	
atc tat aac gcc cag ctg cag gat gct ggg atc tac acc tgc acg gcc	1103
Ile Tyr Asn Ala Gln Leu Gln Asp Ala Gly Ile Tyr Thr Cys Thr Ala	
275 280 285	
cgg aac gtg gct ggg gtc ctg agg gct gat ttc ccg ctg tcg gtg gtc	1151
Arg Asn Val Ala Gly Val Leu Arg Ala Asp Phe Pro Leu Ser Val Val	
290 295 300 305	
agg ggt cat cag gct gca gcc acc tca gag agc agc ccc aat ggc acg	1199
Arg Gly His Gln Ala Ala Ala Thr Ser Glu Ser Ser Pro Asn Gly Thr	
310 315 320	
gct ttc ccg gcg gcc gag tgc ctg aag ccc cca gac agt gag gac tgt	1247
Ala Phe Pro Ala Ala Glu Cys Leu Lys Pro Pro Asp Ser Glu Asp Cys	
325 330 335	
ggc gaa gag cag acc cgc tgg cac ttc gat gcc cag gcc aac aac tgc	1295
Gly Glu Glu Gln Thr Arg Trp His Phe Asp Ala Gln Ala Asn Asn Cys	
340 345 350	
ctg acc ttc acc ttc ggc cac tgc cac cgt aac ctc aac cac ttt gag	1343
Leu Thr Phe Thr Phe Gly His Cys His Arg Asn Leu Asn His Phe Glu	
355 360 365	

acc tat gag gcc tgc atg ctg gcc tgc atg agc ggg ccg ctg gcc gcg	1391
Thr Tyr Glu Ala Cys Met Leu Ala Cys Met Ser Gly Pro Leu Ala Ala	
370 375 380 385	
tgc agc ctg ccc gcc ctg cag ggg ccc tgc aaa gcc tac gcg cct cgc	1439
Cys Ser Leu Pro Ala Leu Gln Gly Pro Cys Lys Ala Tyr Ala Pro Arg	
390 395 400	
tgg gct tac aac agc cag acg ggc cag tgc cag tcc ttt gtc tat ggt	1487
Trp Ala Tyr Asn Ser Gln Thr Gly Gln Cys Gln Ser Phe Val Tyr Gly	
405 410 415	
ggc tgc gag ggc aat ggc aac aac ttt gag agc cgt gag gcc tgt gag	1535
Gly Cys Glu Gly Asn Gly Asn Asn Phe Glu Ser Arg Glu Ala Cys Glu	
420 425 430	
gag tcg tgc ccc ttc ccc agg ggg aac cag cgc tgt cgg gcc tgc aag	1583
Glu Ser Cys Pro Phe Pro Arg Gly Asn Gln Arg Cys Arg Ala Cys Lys	
435 440 445	
cct cgg cag aag ctc gtt acc agc ttc tgt cgc agc gac ttt gtc atc	1631
Pro Arg Gln Lys Leu Val Thr Ser Phe Cys Arg Ser Asp Phe Val Ile	
450 455 460 465	
ctg ggc cga gtc tct gag ctg acc gag gag cct gac tcg ggc cgc gcc	1679
Leu Gly Arg Val Ser Glu Leu Thr Glu Glu Pro Asp Ser Gly Arg Ala	
470 475 480	
ctg gtg act gtg gat gag gtc cta aag gat gag aaa atg ggc ctc aag	1727
Leu Val Thr Val Asp Glu Val Leu Lys Asp Glu Lys Met Gly Leu Lys	
485 490 495	
ttc ctg ggc cag gag cca ttg gag gtc act ctg ctt cac gtg gac tgg	1775
Phe Leu Gly Gln Glu Pro Leu Glu Val Thr Leu Leu His Val Asp Trp	
500 505 510	
gca tgc ccc tgc ccc aac gtg acc gtg agc gag atg ccg ctc atc atc	1823
Ala Cys Pro Cys Pro Asn Val Thr Val Ser Glu Met Pro Leu Ile Ile	
515 520 525	
atg ggg gag gtg gac ggc ggc atg gcc atg ctg cgc ccc gat agc ttt	1871
Met Gly Glu Val Asp Gly Gly Met Ala Met Leu Arg Pro Asp Ser Phe	
530 535 540 545	

gtg ggc gca tcg agt gcc cgc cgg gtc agg aag ctt cgt gag gtc atg 1919  
 Val Gly Ala Ser Ser Ala Arg Arg Val Arg Lys Leu Arg Glu Val Met  
                   550                  555                  560

cac aag aag acc tgt gac gtc ctc aag gag ttt ctt ggc ttg cac tga 1967  
 His Lys Lys Thr Cys Asp Val Leu Lys Glu Phe Leu Gly Leu His \*  
                   565                  570                  575

agccccccac ccctccctgc ccctccctg gccttcttcc acctatccac cccaatgcct 2027  
 ctgagcaaac tgggcgaggt cagattagac aggcttggga cagcaggga acatcaaccg 2087  
 acgtgtcaca gaaaaagcca cagaaggtct cagatcagca tctattcttt ggggttcaata 2147  
 aggggttcat atctttttta gctgaggggg acaagaggag aagtcagtgg acacatggaa 2207  
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 cctggctctc ccagtcaccc tcccctagcc agtctccag caagggttta agagatggcc 2327  
 gctgtgtgct ggtcacagga agtgttgaat ggattggctt gcaaaggggg taggtgggga 2387  
 gagataggag ggcccagggg ctcattgggac acctttccca cagcctcctc gattgctgtg 2447  
 agcagaggcc actcggagtt aggggcatgg gcaatagcaa gctggcggca gaggccagcc 2507  
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 cttgcctctg aggccaccac ggcaccagca gaatacgtat ttcttctcct tggctgcatt 2627  
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 aggaccacag agagatgtta gtcactgccc agttcttaga gcccacacac agataccctc 2747  
 atcccagggc cccagacac accctccgc tggactcaca actgtctgga gtttctgtct 2807  
 gatggatggt gtgctttcat atgccactgg cttccttggg catagatcag aaaaagccc 2867  
 cgggatctgt ttggtagcag gagaaatgaa ggaagatgaa aaagcaggca gggaaagggg 2927  
 tagtaaagga ctgagagagg agggaggtgg ctggagaagg aaaaggaaca ttgctcgtg 2987  
 ctcccatctg gtggcggcct caggaaccca cggaacctg gaaggaggct ctttgtgaga 3047  
 cctgggcaaa ggatggggca gctcgtcgtg gatttttttg tgtttccagg cttcctgtgt 3107  
 gatcctggcc ctccggccgc tagagagagg attgggaaac cccactgtca gctctgcac 3167  
 tgccccact accctcctct gccctattct gtccctgccc ctccaagctg aagaaggtcc 3227  
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 tagtatcaac tgca 3301

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<211> 576

<212> PRT

<213> Homo sapiens

<400> 2

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 Ala Ala Leu Leu Leu Leu Leu Leu Leu Gly Val Pro Pro Arg Ser  
                   20                  25                  30

Leu Ala Leu Pro Pro Ile Arg Tyr Ser His Ala Gly Ile Cys Pro Asn  
 35 40 45  
 Asp Met Asn Pro Asn Leu Trp Val Asp Ala Gln Ser Thr Cys Arg Arg  
 50 55 60  
 Glu Cys Glu Thr Asp Gln Glu Cys Glu Thr Tyr Glu Lys Cys Cys Pro  
 65 70 75 80  
 Asn Val Cys Gly Thr Lys Ser Cys Val Ala Ala Arg Tyr Met Asp Val  
 85 90 95  
 Lys Gly Lys Lys Gly Pro Val Gly Met Pro Lys Glu Ala Thr Cys Asp  
 100 105 110  
 His Phe Met Cys Leu Gln Gln Gly Ser Glu Cys Asp Ile Trp Asp Gly  
 115 120 125  
 Gln Pro Val Cys Lys Cys Lys Asp Arg Cys Glu Lys Glu Pro Ser Phe  
 130 135 140  
 Thr Cys Ala Ser Asp Gly Leu Thr Tyr Tyr Asn Arg Cys Tyr Met Asp  
 145 150 155 160  
 Ala Glu Ala Cys Ser Lys Gly Ile Thr Leu Ala Val Val Thr Cys Arg  
 165 170 175  
 Tyr His Phe Thr Trp Pro Asn Thr Ser Pro Pro Pro Pro Glu Thr Thr  
 180 185 190  
 Met His Pro Thr Thr Ala Ser Pro Glu Thr Pro Glu Leu Asp Met Ala  
 195 200 205  
 Ala Pro Ala Leu Leu Asn Asn Pro Val His Gln Ser Val Thr Met Gly  
 210 215 220  
 Glu Thr Val Ser Phe Leu Cys Asp Val Val Gly Arg Pro Arg Pro Glu  
 225 230 235 240  
 Ile Thr Trp Glu Lys Gln Leu Glu Asp Arg Glu Asn Val Val Met Arg  
 245 250 255  
 Pro Asn His Val Arg Gly Asn Val Val Val Thr Asn Ile Ala Gln Leu  
 260 265 270  
 Val Ile Tyr Asn Ala Gln Leu Gln Asp Ala Gly Ile Tyr Thr Cys Thr  
 275 280 285  
 Ala Arg Asn Val Ala Gly Val Leu Arg Ala Asp Phe Pro Leu Ser Val  
 290 295 300  
 Val Arg Gly His Gln Ala Ala Ala Thr Ser Glu Ser Ser Pro Asn Gly  
 305 310 315 320  
 Thr Ala Phe Pro Ala Ala Glu Cys Leu Lys Pro Pro Asp Ser Glu Asp  
 325 330 335  
 Cys Gly Glu Glu Gln Thr Arg Trp His Phe Asp Ala Gln Ala Asn Asn  
 340 345 350  
 Cys Leu Thr Phe Thr Phe Gly His Cys His Arg Asn Leu Asn His Phe  
 355 360 365

Glu Thr Tyr Glu Ala Cys Met Leu Ala Cys Met Ser Gly Pro Leu Ala  
 370 375 380  
 Ala Cys Ser Leu Pro Ala Leu Gln Gly Pro Cys Lys Ala Tyr Ala Pro  
 385 390 395 400  
 Arg Trp Ala Tyr Asn Ser Gln Thr Gly Gln Cys Gln Ser Phe Val Tyr  
 405 410 415  
 Gly Gly Cys Glu Gly Asn Gly Asn Asn Phe Glu Ser Arg Glu Ala Cys  
 420 425 430  
 Glu Glu Ser Cys Pro Phe Pro Arg Gly Asn Gln Arg Cys Arg Ala Cys  
 435 440 445  
 Lys Pro Arg Gln Lys Leu Val Thr Ser Phe Cys Arg Ser Asp Phe Val  
 450 455 460  
 Ile Leu Gly Arg Val Ser Glu Leu Thr Glu Glu Pro Asp Ser Gly Arg  
 465 470 475 480  
 Ala Leu Val Thr Val Asp Glu Val Leu Lys Asp Glu Lys Met Gly Leu  
 485 490 495  
 Lys Phe Leu Gly Gln Glu Pro Leu Glu Val Thr Leu Leu His Val Asp  
 500 505 510  
 Trp Ala Cys Pro Cys Pro Asn Val Thr Val Ser Glu Met Pro Leu Ile  
 515 520 525  
 Ile Met Gly Glu Val Asp Gly Gly Met Ala Met Leu Arg Pro Asp Ser  
 530 535 540  
 Phe Val Gly Ala Ser Ser Ala Arg Arg Val Arg Lys Leu Arg Glu Val  
 545 550 555 560  
 Met His Lys Lys Thr Cys Asp Val Leu Lys Glu Phe Leu Gly Leu His  
 565 570 575

&lt;210&gt; 3

&lt;211&gt; 1728

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; degenerate sequence

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1728)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 3

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ytnytnytny	tnytnytnng	ngtnccnccn	mgnwsnytn	cnytnccncc	nathmgntay	120
wsncaygcng	gnathtgycc	naaygayatg	aayccnaayy	tntgggtnga	ygcncarwsn	180



acntgymgrn	gngartgyga	racngaycar	gartgygara	cntaygaraa	rtgytgyccn	240
aaygtntgyg	gnacnaarws	ntgygtngcn	gcnmgntaya	tggaygtnaa	rggnaaraar	300
ggncngtng	gnatgccnaa	rgargcnacn	tgygaycayt	tyatgtgyyt	ncarcarggn	360
wsngartgyg	ayathtgga	yggncarccn	gtntgyaart	gyaargaymg	ntgygaraar	420
garccnwsnt	tyacntgygc	nwsngayggn	ytnacntayt	ayaaymgntg	ytayatggay	480
gcngargcnt	gywsnaargg	nathacnytn	gcngtngtna	cntgymgnta	ycayttyacn	540
tggccnaaya	cnwsnccncc	nccnccngar	acnacnatgc	ayccnacnac	ngcnwsnccn	600
garacnccng	arytngayat	ggcngcnccn	gcnytnytna	ayaayccngt	ncaycarwsn	660
gtnacnatgg	ngaracngt	nwsnttytn	tgygaygtng	tnggnmgnc	nmgnccngar	720
athacntggg	araarcaryt	ngargaymg	garaaygtng	tnatgmgncc	naaycaygt	780
mgnggnaayg	tngtngtnac	naayathgcn	carytngtna	thtayaaygc	ncarytnar	840
gaygcnggna	thtayacntg	yacngcnmg	aaygtngcng	gngtnytnmg	ngcngaytty	900
ccnytnwsng	tngtnmgngg	ncaycargcn	gcngcnacnw	sngarwsnws	nccnaayggn	960
acngcnttyc	cngcngcnga	rtgyytnaar	ccnccngayw	sngargaytg	yggngargar	1020
caracnmgt	ggcayttyga	ygcncargcn	aayaaytgyy	tnacnttyac	nttyggncay	1080
tgycaymgna	ayytnaayca	ytygaracn	taygargcnt	gyatgytngc	ntgyatgwsn	1140
ggncnytnng	cngcntgyws	nytnccngcn	ytncarggnc	cntgyaargc	ntaygcncn	1200
mgntgggcnt	ayaaywsnca	racnggncar	tgycarwsnt	tygtntaygg	nggntgygar	1260
ggnaayggn	ayaayttyga	rwsnmngar	gcntgygarg	arwsntgycc	nttyccnmgn	1320
ggnaaycarm	gntgymngc	ntgyaarccn	mgncaraary	tngtnacnws	nttytgymgn	1380
wsngayttyg	tnathytnng	nmngntnwsn	garytnacng	argarccnga	ywsnggnmg	1440
gcnytngtna	cngtngayga	rgtnytnaar	gaygaraara	tgggnytnaa	rttyytnngn	1500
cargarccny	tngargtnac	nytnytnac	gtngaytggg	cntgyccntg	yccnaaygt	1560
acngtnwsng	aratgccnyt	nathathatg	ggngargtng	ayggnggnat	ggcnatgytn	1620
mgncngayw	snttygtngg	ngcnwsnwsn	gcnmgnmng	tnmgnaaryt	nmngngargtn	1680
atgcayaara	aracntgyga	ygtnytnaar	garttyytng	gnytnac		1728

&lt;210&gt; 4

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; kunitz domain 1

&lt;221&gt; VARIANT

&lt;222&gt; (2)...(2)

&lt;223&gt; Xaa is any amino acid except Asp, Cys, Gly, His, Met, Pro or

Tyr

&lt;221&gt; VARIANT

&lt;222&gt; (3)...(3)

&lt;223&gt; Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala, Pro or Lys

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Tyr, or Trp

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<223> Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile

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<222> (17)...(17)  
<223> Xaa is Phe, Tyr, Ile, Trp or Leu

<221> VARIANT  
<222> (18)...(18)  
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<221> VARIANT  
<222> (19)...(19)  
<223> Xaa is Tyr or Phe

<221> VARIANT  
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<221> VARIANT

<222> (25)...(25)

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or Val

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<221> VARIANT

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<221> VARIANT

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<221> VARIANT

<222> (32)...(32)

<223> Xaa is Ser, Gly or Thr

<221> VARIANT

<222> (33)...(33)

<223> Xaa is Gly, Ile or His

<221> VARIANT

<222> (35)...(35)

<223> Xaa is Gly, Lys, Arg, Pro, Gln, Leu, Glu, Asn, Met or His

<221> VARIANT

<222> (36)...(36)

<223> Xaa is Gly, Lys, Ala or Arg

<221> VARIANT

<222> (37)...(37)

<223> Xaa is Asn, Lys or Ser

<221> VARIANT

<222> (38)...(38)

<223> Xaa is any amino acid except Cys, His, Ile, Phe, Pro, Thr, Trp, Tyr or Val

<221> VARIANT

<222> (39)...(39)

<223> Xaa is Asn or Tyr

<221> VARIANT

<222> (40)...(40)

<223> Xaa is Arg, Asn, Lys, Gln, Val or His

<221> VARIANT

<222> (41)...(41)

<223> Xaa is Phe, Tyr or Asp

<221> VARIANT

<222> (42)...(42)

<223> Xaa is any amino acid except Cys, Gln, Gly, Phe or Trp

<221> VARIANT

<222> (43)...(43)

<223> Xaa is Thr, Ser, Arg, Lys or Asp

<221> VARIANT

<222> (44)...(44)

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<221> VARIANT

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<221> VARIANT

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<221> VARIANT

<222> (48)...(48)

<223> Xaa is any amino acid except Ala, Cys, Gly, Phe, Pro, Ser, Thr, Trp or Tyr

<221> VARIANT

<222> (49)...(49)

<223> Xaa is any amino acid except Cys, Ile, Met, Phe, Pro, Ser, Trp  
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<221> VARIANT

<222> (50)...(50)

<223> Xaa is Thr, Ala, Val, Ile, Phe, Leu, Met, Lys, Tyr or Arg

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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20				25						30		
Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa
			35				40						45		
Xaa	Xaa	Cys													
			50												

<210> 5

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> kunitz domain 2

<221> VARIANT

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<223> Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile

<221> VARIANT

<222> (17)...(17)

<223> Xaa is Phe, Tyr, Ile, Trp or Leu

<221> VARIANT

<222> (18)...(18)

<223> Xaa is Gln, His, Phe, Trp, Asn or Ala

<221> VARIANT

<222> (19)...(19)

<223> Xaa is Tyr or Phe

<221> VARIANT  
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<223> Xaa is Lys, Asn, Ser or Asp

<221> VARIANT  
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<223> Xaa is any amino acid except Asp, Cys, Glu, His or Tyr

<221> VARIANT  
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<221> VARIANT  
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Trp, Tyr or Val

<221> VARIANT  
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<221> VARIANT  
<222> (28)...(28)  
<223> Xaa is any amino acid except Asp, Cys, His, Ile, Phe, Trp or  
Tyr

<221> VARIANT  
<222> (29)...(29)  
<223> Xaa is Phe or Tyr

<221> VARIANT  
<222> (30)...(30)  
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<221> VARIANT

<222> (31)...(31)

<223> Xaa is Tyr, Trp, Phe or Asp

<221> VARIANT

<222> (32)...(32)

<223> Xaa is Gly or Thr

<221> VARIANT

<222> (33)...(33)

<223> Xaa is Gly or Ile

<221> VARIANT

<222> (35)...(35)

<223> Xaa is Gly, Lys, Arg, Pro, Gln, Leu, Glu, Asn or Met

<221> VARIANT

<222> (36)...(36)

<223> Xaa is Gly, Lys or Ala

<221> VARIANT

<222> (37)...(37)

<223> Xaa is Asn, Lys or Ser

<221> VARIANT

<222> (38)...(38)

<223> Xaa is any amino acid except Cys, His, Ile, Phe, Pro, Thr, Trp,  
Tyr or Val

<221> VARIANT

<222> (39)...(39)

<223> Xaa is Asn or Tyr

<221> VARIANT

<222> (40)...(40)

<223> Xaa is Arg, Asn, Lys, Gln or Val

<221> VARIANT

<222> (41)...(41)

<223> Xaa is Phe, Tyr or Asp

<221> VARIANT

<222> (42)...(42)

<223> Xaa is any amino acid except Cys, Gln, Gly, Phe or Trp

<221> VARIANT

<222> (43)...(43)

<223> Xaa is Thr, Ser, Arg, Lys or Asp

<221> VARIANT

<222> (44)...(44)

<223> Xaa is Ile, Leu, Trp, Arg, Lys, Thr, Glu, Ala, Gln or Val

<221> VARIANT

<222> (45)...(45)

<223> Xaa is Glu, Asp, Ala, His, Met, Val, Gln, Lys, Arg or Pro

<221> VARIANT

<222> (46)...(46)

<223> Xaa is Glu, Lys, Gln, Asp, Ala, Tyr or Ser

<221> VARIANT

<222> (48)...(48)

<223> Xaa is any amino acid except Ala, Cys, Gly, Phe, Pro, Ser, Thr, Trp or Tyr

<221> VARIANT

<222> (49)...(49)

<223> Xaa is any amino acid except Cys, Ile, Met, Phe, Pro, Ser, Trp or Tyr

<221> VARIANT

<222> (50)...(50)

<223> Xaa is Thr, Ala, Val, Ile, Phe, Leu, Met, Lys, Tyr, Arg or Ser

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Cys Ser Leu Pro Ala Leu Gln Gly Pro Cys Lys Ala Tyr Ala Pro Xaa

1

5

10

15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa

20

25

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Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa

35

40

45

Xaa Xaa Cys

50

<210> 6



16

<211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 6  
 Glu Tyr Pro Met Glu  
 1 5

<210> 7  
 <211> 51  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> kunitz motif

<221> VARIANT  
 <222> (1)...(51)  
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 1 5 10 15  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa  
 35 40 45  
 Xaa Xaa Cys  
 50

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